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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:25:12 ; Search time 58.0357 Seconds
(without alignments)
888.869 Million cell updates/sec

Title: US-09-805-427a-2
Perfect score: 1745
Sequence: 1 MTDSVKIRAWGRRLMIGTA.....YGAQLNAMKGLQSLGAG 325

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1078588

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database : A Geneseq 19Jun03:*

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1745	100.0	325	18	AAW18164
2	1745	100.0	325	19	AAW63032
3	1745	100.0	325	19	AAW46776
4	1745	100.0	325	20	AAW14853
5	1745	100.0	325	22	AAW47556
6	1745	100.0	325	23	ABW73459
7	1745	100.0	325	23	AAW50730
8	1745	100.0	325	24	ABU56406
9	1706	97.8	323	23	ABW73461

10	1699	97.4	323	20	AAW14855	Antigen 85B protei
11	1602	91.8	325	12	AAW10486	Tuberculin active
12	1595	91.4	325	11	AAW08099	Mycobacterium deri
13	1550	88.8	403	19	AAW72943	Mycobacterium tube
14	1550	88.8	403	20	AAW21963	Amino acid sequenc
15	1550	88.8	404	19	AAW72942	Mycobacterium tube
16	1550	88.8	404	20	AAW21962	Amino acid sequenc
17	1522	87.2	330	19	AAW46777	Tuberculin active
18	1510	86.5	283	10	AAW90109	Antigen 85B protei
19	1454	83.3	327	20	AAW14851	M leprae 85B prote
20	1454	83.3	327	23	ABW73457	Mycobacterium-orig
21	1437	82.3	285	23	ABW83662	Mycobacterium tube
22	1407	80.6	337	24	ABU56407	Mycobacterium tube
23	1407	80.6	338	18	AAW18165	Mycobacterium tube
24	1407	80.6	338	19	AAW63033	Mycobacterium tube
25	1407	80.6	338	20	AAW14852	Antigen 85A protei
26	1407	80.6	338	20	AAW14854	Antigen 85A protei
27	1407	80.6	338	22	ABW47555	Ag85A. Mycobacter
28	1407	80.6	338	22	ABW82789	Mycobacterium tube
29	1407	80.6	338	23	ABW73458	M tuberculosis 85A
30	1407	80.6	338	23	ABW73460	M bovis 85A protei
31	1407	80.6	338	23	AAW50729	Mycobacterium tube
32	1401	80.3	338	12	AAW11296	Recombinant M.tube
33	1362.5	78.1	353	12	AAW11295	Recombinant M.tube
34	1335.5	76.5	330	20	AAW14850	Antigen 85A protei
35	1335.5	76.5	330	23	AAW73456	Mycobacterium tube
36	1323	75.8	295	23	AAW50759	M tuberculosis an
37	1322	75.8	302	21	AAW6926	M. tuberculosis an
38	1198	68.7	340	22	ABW47557	Ag85C. Mycobacter
39	1198	68.7	340	23	AAW50731	Mycobacterium tube
40	1195	68.5	340	13	AAW26167	85-C. Mycobacteri
41	1195	68.5	340	20	AAW14857	Antigen 85C protei
42	1195	68.5	340	23	ABW73463	M tuberculosis 85C
43	1179	67.6	326	19	AAW60112	Mycobacterium vacc
44	1179	67.6	326	20	AAW14858	M. vaccae antigen
45	1179	67.6	326	23	ABW73464	M vaccae antigen 8
46	1170	67.0	333	20	AAW14856	Antigen 85C protei
47	1170	67.0	333	23	ABW73462	M leprae 85C prote
48	1151.5	66.0	334	19	AAW60114	Mycobacterium vacc
49	1151.5	66.0	334	20	AAW14860	M. vaccae antigen
50	1151.5	66.0	334	23	ABW73466	M. vaccae antigen 8
51	644	36.9	161	19	AAW60113	Mycobacterium vacc
52	644	36.9	161	20	AAW14859	M. vaccae antigen
53	644	36.9	161	23	ABW73465	M. vaccae antigen 8
54	637	36.5	161	19	AAW60127	Mycobacterium vacc
55	637	36.5	161	23	ABW73479	M. vaccae GV-4P par
56	636	36.4	161	20	AAW14908	Amino acid sequenc
57	636	36.4	161	23	ABW73514	Amino acid sequenc
58	635	36.4	160	20	AAW14873	Mycobacterium tube
59	519	29.7	239	18	AAW18162	Mycobacterium tube
60	519	29.7	239	19	AAW72899	Mycobacterium tube
61	519	29.7	239	19	AAW63037	Mycobacterium tube
62	519	29.7	239	20	AAW21916	Amino acid sequenc
63	474	27.2	657	14	AAW32657	PS1 protein from C
64	470	26.9	657	22	AAW92916	C glutamicum prote
65	415	23.8	341	22	AAW92919	C glutamicum prote
66	397	22.8	114	23	ABP03110	Human ORFX protein
67	303.5	17.4	411	22	AAW90895	C glutamicum prote
68	279	16.0	462	22	AAW90774	C glutamicum prote
69	277	15.9	483	22	AAW92137	C glutamicum prote
70	263	15.1	358	19	AAW56155	Aa cell surface la
71	262	15.0	626	20	AAW98010	BCG Ag85B antigen-
72	262	15.0	626	24	ABU08321	M. bovis Ag85B-L.
73	238.5	13.7	365	22	AAW90128	C glutamicum prote
74	209	12.0	40	16	AAW85683	30 kD M.tuberculos
75	209	12.0	40	16	AAW85687	Extended N-termina
76	209	12.0	40	17	AAW92883	Mycobacterium 30 k
77	209	12.0	40	18	AAW18191	N-terminal sequenc
78	209	12.0	40	19	AAW75579	M. tuberculosis 30
79	209	12.0	40	19	AAW75567	M. tuberculosis 30
80	209	12.0	40	24	ABW74416	M. tuberculosis ex
81	209	12.0	40	24	ABW74424	M. tuberculosis ex
82	209	12.0	40	24	ABU56331	M. tuberculosis ex

83 209 12.0 40 24 ABUS6332 M. tuberculosis ex
84 209 12.0 40 24 ABUS6343 M. tuberculosis ex
85 203 11.6 39 22 AAE05566 N-terminal amino a
86 202 11.6 40 18 AAW18192 N-terminal sequenc
87 202 11.6 40 24 ABUS6344 M. tuberculosis ex
88 201 11.5 40 19 AAW75569 M. tuberculosis 32
89 198 11.3 40 19 AAW75568 M. tuberculosis 32
90 198 11.3 40 24 ABG74433 M. tuberculosis ex

ALIGNMENTS

RESULT 1

ID AAW18164 standard; Protein; 325 AA.
XX AAW18164;
AC AAW18164;
DT 13-AUG-1997 (first entry)
DE Mycobacterium tuberculosis extracellular 30KD protein.
XX Vaccine, vaccinating agent; M.tuberculosis; pathogen; bacteria;
KW virus; fungus; protozoan; HIV.
XX Mycobacterium tuberculosis.
OS
PH Key Location/Qualifiers
FT Protein 41..325
FT /label= Mature
PN WO9637219-Al.
XX
XX 28-NOV-1996.
PD
XX
XX 23-MAY-1996; 96WO-US07781.
XX
XX 06-DEC-1995; 95US-0568357.
XX 23-MAY-1995; 95US-0447398.
XX 20-OCT-1995; 95US-0545926.
XX 31-OCT-1995; 95US-0551149.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Harth G, Horwitz MA;
XX
XX WPI; 1997-020936/02.
XX N-PSDB; AAT71598.
XX
XX Vaccines derived from M.tuberculosis major abundant extracellular
XX proteins - are easy to prepare and less toxic than conventional
XX killed or attenuated vaccines, useful for protecting against or
XX treating Mycobacterial infections
XX
XX Claim 1; Page 35-36; 193pp; English.
XX
XX A vaccinating agent for promoting an immune response in a mammal
XX against Mycobacterium pathogens comprises at least one majorly abundant
XX extracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45,
XX 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their
XX analogues, homologues and subunits. The present sequence represents the
XX 30 kD protein. The vaccinating agents are used to protect against (or
XX to treat existing) infections by Mycobacterium (especially M.
XX tuberculosis) while the epitopes can also be used to detect presence
XX of an immune response to a Mycobacterium pathogen. The vectors,
XX containing the DNA for the extracellular proteins, are used to transform
XX cells for production of recombinant DNA molecules. More generally the
XX DNA from other pathogens can be used in vaccines, e.g. against other
XX bacteria, viruses, fungi and protozoa. Since different combinations of
XX DNA can be used, a wide range of effective compositions can be produced.
XX They generate a response against the antigens most often found on
XX infected cells during the infection, regardless of the strength or

CC specificity of the immune response. The vaccines are easy to produce
CC and less toxic than known killed or attenuated vaccines, so can be given
CC to immunocompromised subjects, e.g. those with HIV infection.
XX
SQ Sequence 325 AA;
Query Match 100.0%; Score 1745; DB 18; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.2e-143; Indels 0; Gaps 0;
Matches 325; Conservative 0; Mismatches 0;
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Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSPYS 120
Db 61 DIKVFQSGGNNSPAVILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSPYS 120
QY 121 DWSPACGKAGCQTYKWETFLTSELPWLSANRAVKPTGSAAGISMAAGSSAMILLAAVHP 180
Db 121 DWSPACGKAGCQTYKWETFLTSELPWLSANRAVKPTGSAAGISMAAGSSAMILLAAVHP 180
QY 181 QQFIYAGSLSLALDPSQGMGFSLLGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
Db 181 QQFIYAGSLSLALDPSQGMGFSLLGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
QY 241 VANNTRLWVYCGNGTNPNELGANTPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPENG 300
Db 241 VANNTRLWVYCGNGTNPNELGANTPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPENG 300
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQLNAMKGDLOSSLGAG 325

RESULT 2

AAW63032
ID AAW63032 standard; Protein; 325 AA.
XX
AC AAW63032;
XX
DT 23-OCT-1998 (first entry)
XX
DE Mycobacterium tuberculosis 30 kD protein sequence.
XX
KW Mycobacterium tuberculosis; vaccination; extracellular product;
KW immunodominant epitope; interleukin-12; MF59; immune response;
KW opsonising humoral response; intracellular pathogen.
XX
OS Mycobacterium tuberculosis.
XX
FN WO9831388-Al.
XX
PD 23-JUL-1998.
XX
XX 15-JAN-1998; 98WO-US00942.
XX
XX 21-JAN-1997; 97US-0786533.
XX (REGC) UNIV CALIFORNIA.
XX
XX Harth G, Horwitz MA, Lee B;
XX WPI; 1998-413815/35.
XX N-PSDB; AAV42595.
XX
XX Vaccines against Mycobacterium containing major extracellular
XX proteins - used to, e.g. induce protective and therapeutic immune
XX responses, and for detecting an immune response
XX
XX Example 2; Pages 37-38; 236pp; English.
XX
XX This represents a Mycobacterium tuberculosis 30 kD protein. The invention

CC provides an agent for vaccinating mammals against Mycobacterium. The
 CC agent comprises at least one of the major abundant extracellular 110,
 CC 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 KD proteins of
 CC M. tuberculosis, or at least 1 of their immunodominant epitopes and
 CC interleukin-12 (IL-12) or MF59 as adjuvants. The agent containing the
 CC nucleic acid encoding the extracellular products are used to raise a
 CC protective or therapeutic immune response against Mycobacterium,
 CC specifically M. tuberculosis. The immunodominant epitopes can also be
 CC used (typically in a cutaneous hypersensitivity test) to detect an
 CC immune response to vaccination. Preparation of the agent does not require
 CC selection of the most immunogenic products, so large scale production and
 CC purification are easy, resulting in a consistent, standardised
 CC formulation, having lower toxicity than killed or attenuated vaccines.
 CC The agents provide a rapid and effective response (including a strong
 CC cell-mediated component) and are safe even in immunocompromised subjects.
 CC They prevent development of an opsonising humoral response that might
 CC spread intracellular pathogens.

XX SQ Sequence 325 AA;
 Query Match 100.0%; Score 1745; DB 19; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.2e-143;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
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 DB 61 DIKVPQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
 QY 121 DWSPACGKAGCCTYKWTFTLSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAHP 180
 DB 121 DWSPACGKAGCCTYKWTFTLSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAHP 180
 QY 181 QQFIYAGSLALLDPQSGMGPSLIGLWAGDAGGYKAADMWGPDSPDPAWERNDPTQIIPKL 240
 DB 181 QQFIYAGSLALLDPQSGMGPSLIGLWAGDAGGYKAADMWGPDSPDPAWERNDPTQIIPKL 240
 QY 241 VANNTRELWYCGNGTPELGGANI PAEFLNFVRSSNLKFDQDAYNAAGGHNAVFNPFPNG 300
 DB 241 VANNTRELWYCGNGTPELGGANI PAEFLNFVRSSNLKFDQDAYNAAGGHNAVFNPFPNG 300
 QY 301 THSWEYWGALNMGKGLDQSSLGAG 325
 DB 301 THSWEYWGALNMGKGLDQSSLGAG 325

RESULT 3
 AAW46776
 ID AAW46776 standard; peptide; 325 AA.
 AC AAW46776;

XX 09-JUL-1998 (first entry)
 DE Amino acid sequence of alpha antigen of Mycobacterium tuberculosis.
 XX Alpha antigen; mycobacterial disease; monoclonal antibody; detection;
 KW Mycobacteria; Mycobacterium avium; intracellular.
 XX Mycobacterium tuberculosis.
 OS

XX WO9804918-A1.
 XX 05-FEB-1998.
 XX 24-JUN-1997; 97WO-US13235.
 XX 26-JUL-1996; 96US-0690347.
 XX (UYCA-) UNIV CASE WESTERN RESERVE.
 PA

XX Wallis RS;
 DR WPI; 1998-130832/12.

PT Detection of mycobacteria - using a monoclonal antibody directed
 PT against a portion of the alpha antigen, and detection of complexes
 PT formed

XX Claim 11; Fig 19; 105pp; English.

XX The present sequence represents the alpha antigen of Mycobacterium
 CC tuberculosis. The alpha antigen is an abundantly produced, secreted 30
 CC kilodalton mycobacterial protein involved in mycolic acid synthesis. It
 CC is an useful indicator of mycobacterial disease as it can account for up
 CC to 20% of the protein content of spent mycobacterial culture medium. In
 CC addition, homologous alpha proteins exist for most species of
 CC Mycobacteria. Monoclonal antibodies were produced against the present
 CC sequence and its fragments. These can be used for the detection of
 CC Mycobacteria in a test sample. The method can be used for the detection
 CC of Mycobacteria such as M. tuberculosis, M. avium and M. intracellulare.
 CC The method can be used to monitor the progression of therapy in
 CC individuals infected with Mycobacteria.

XX SQ Sequence 325 AA;

Query Match 100.0%; Score 1745; DB 19; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.2e-143;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
 QY 61 DIKVPQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
 DB 61 DIKVPQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
 QY 121 DWSPACGKAGCCTYKWTFTLSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAHP 180
 DB 121 DWSPACGKAGCCTYKWTFTLSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAHP 180
 QY 181 QQFIYAGSLALLDPQSGMGPSLIGLWAGDAGGYKAADMWGPDSPDPAWERNDPTQIIPKL 240
 DB 181 QQFIYAGSLALLDPQSGMGPSLIGLWAGDAGGYKAADMWGPDSPDPAWERNDPTQIIPKL 240
 QY 241 VANNTRELWYCGNGTPELGGANI PAEFLNFVRSSNLKFDQDAYNAAGGHNAVFNPFPNG 300
 DB 241 VANNTRELWYCGNGTPELGGANI PAEFLNFVRSSNLKFDQDAYNAAGGHNAVFNPFPNG 300
 QY 301 THSWEYWGALNMGKGLDQSSLGAG 325
 DB 301 THSWEYWGALNMGKGLDQSSLGAG 325

RESULT 4
 AAY14853
 ID AAY14853 standard; protein; 325 AA.
 XX AAY14853;
 AC AAY14853;
 XX 25-OCT-1999 (first entry)
 DE Antigen 85B protein from M. tuberculosis.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 XX squamous cell carcinoma; melanoma.
 XX Mycobacterium tuberculosis.


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Db 121 DWSPACGKAGCQTYKWTFTLSLPOWLSANRAVKPTGSAAGLSMAGSSAMTAAAYHP 180
QY 181 QQFIYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQQIPKL 240
Db 181 QQFIYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQQIPKL 240
QY 241 VANNTRLWVYCGNGTNPNEGANIIPAEFLENFVRSSNLKFDAYNAAGHNAVFPPNG 300
Db 241 VANNTRLWVYCGNGTNPNEGANIIPAEFLENFVRSSNLKFDAYNAAGHNAVFPPNG 300
QY 301 THSWEYWGAGLNAMKGDQLQSSLGAG 325
Db 301 THSWEYWGAGLNAMKGDQLQSSLGAG 325

RESULT 6
ABB73459
ID ABB73459 standard; Protein; 325 AA.
XX AC ABB73459;
XX DT 08-APR-2002 (first entry)
XX DE M tuberculosis 85B protein SEQ ID NO: 33.
XX KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
XX KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
XX KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
XX KW Th2 immune response; immunomodulatory.
XX OS Mycobacterium tuberculosis.
XX PN US6328978-B1.
XX PD 11-DEC-2001.
XX PF 02-JUN-1999; 99US-0324542.
XX PR 23-DEC-1997; 97US-0997080.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Watson JD, Tan PLJ, Prestidge R;
XX WPI; 2002-138361/18.
XX Inhibiting skin inflammation associated with skin disorder e.g.
XX psoriasis, by administering composition comprising delipidated and
XX deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
XX culture filtrate -
XX Example 5; Column 61-62; 116pp; English.
XX The present invention relates to a method of inhibiting skin inflammation
XX associated with a skin disorder selected from psoriasis, atopic
XX dermatitis and allergic contact dermatitis, which involves administering
XX a composition containing delipidated and deglycolipidated Mycobacterium
XX vaccae cells or M. vaccae culture filtrate. The skin disorder to be
XX treated may also include alopecia areata, and skin cancers such as basal
XX cell carcinoma, squamous cell carcinoma and melanoma. The composition
XX acts by inhibiting the Th2 immune response. The present sequence is a
XX protein described in the exemplification of the invention.
XX Sequence 325 AA;
XX Query Match 100.0%; Score 1745; DB 23; Length 325;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-143;
XX Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDVSKIRAWGRRLMIGTAAAVVLGVLGAGTAAGAFSRPGLPVEYLOVPSMGR 60
Db 1 MTDVSKIRAWGRRLMIGTAAAVVLGVLGAGTAAGAFSRPGLPVEYLOVPSMGR 60

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QY 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSFFS 120
Db 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSFFS 120
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Db 121 DWSPACGKAGCQTYKWTFTLSLPOWLSANRAVKPTGSAAGLSMAGSSAMTAAAYHP 180
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QY 241 VANNTRLWVYCGNGTNPNEGANIIPAEFLENFVRSSNLKFDAYNAAGHNAVFPPNG 300
Db 241 VANNTRLWVYCGNGTNPNEGANIIPAEFLENFVRSSNLKFDAYNAAGHNAVFPPNG 300
QY 301 THSWEYWGAGLNAMKGDQLQSSLGAG 325
Db 301 THSWEYWGAGLNAMKGDQLQSSLGAG 325

RESULT 7
AAM50730
ID AAM50730 standard; Protein; 325 AA.
XX AC AAM50730;
XX DT 18-APR-2002 (first entry)
XX DE Mycobacterium tuberculosis immunodominant Mtb protein FbpB Ag85B.
XX KW Mtb; FbpB; Ag85B; immunogen; mycobacteria; immunisation; vaccine.
XX OS Mycobacterium tuberculosis.
XX FH Key Location/Qualifiers
XX FT Peptide 1..40
XX FT /label= Signal peptide
XX FT /note= "SEC-dependent signal secretion sequence"
XX FT Protein 41..325
XX FT /label= Mature protein
XX PN WO200204018-A2.
XX PD 17-JAN-2002.
XX PF 10-JUL-2001; 2001WO-US21717.
XX PR 10-JUL-2000; 2000US-217646P.
XX PA (COLS ) UNIV COLORADO STATE RES FOUND.
XX PI Orme IM, Belisle JT;
XX WPI; 2002-164602/21.
XX Vaccine for boosting immunity to mycobacteria when administered in
XX mid-life in a subject who has been vaccinated in childhood with
XX Bacillus Calmette-Guerrin, has purified proteins from mycobacterium
XX tuberculosis -
XX Claim 8; Page 17; 61pp; English.
XX The present sequence is that of the Mycobacterium tuberculosis
XX (Mtb) strain H37Rv gene Rv1886c product, designated FbpB Ag85B.
XX This is one of 31 immunodominant secreted or cytosolic Mtb proteins
XX of strain H37Rv (see AAM50729-59) discovered through the use of
XX 2-dimensional liquid phase electrophoresis coupled with an in vitro
XX interferon-gamma assay and liquid chromatography-mass spectrometry.
XX The immunogens stimulate a strong interferon-gamma response from
XX T cells of M. tuberculosis infected mice. The invention provides
XX vaccine compositions for boosting immunity to mycobacteria when

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CC administered in mid-life to a subject who has been vaccinated
 CC neonatally or in early childhood with ECG and in whom protective
 CC immunity has waned. The vaccine compositions comprise 1 or more
 CC of the 31 purified immunogenic proteins. When used as immunogens,
 CC the secreted Mtb proteins lack the secreted signal sequence. A
 CC preferred protein is Ag85A (see AAM50759), the secreted product of
 CC the RV3084v gene.

XX SQ Sequence 325 AA;
 Query Match 100.0%; Score 1745; DB 23; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.2e-143;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFRRPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFRRPGLPVEYLQVPSMGR 60
 QY 61 DIKVOFSGGNNSPAVLLDGLRAODDYGNDINTPAFEWYQSLGSLVMPVGGSSFFS 120
 DB 61 DIKVOFSGGNNSPAVLLDGLRAODDYGNDINTPAFEWYQSLGSLVMPVGGSSFFS 120
 QY 121 DWSPACGKAGCQYKWTETLTSELPOWLSANRAVKPTGSAIIGLSMAGSSAMILAAVHP 180
 DB 121 DWSPACGKAGCQYKWTETLTSELPOWLSANRAVKPTGSAIIGLSMAGSSAMILAAVHP 180
 QY 181 QQFIYAGSLSALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPTQOIPL 240
 DB 181 QQFIYAGSLSALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPTQOIPL 240
 QY 241 VANNTRLWVYCGNGTPELNGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVFPPNG 300
 DB 241 VANNTRLWVYCGNGTPELNGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVFPPNG 300
 QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
 DB 301 THSWEYGAQLNAMKGDLOSSLGAG 325

RESULT 8
 ABUS6406
 ID ABUS6406 standard; Protein; 325 AA.
 AC ABUS6406;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis 30kDa protein.
 KW Antibacterial; tuberculosis; vaccine; gene therapy; 30kDa protein.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US2002131975-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 14-SEP-2001; 2001US-0953510.
 XX
 PR 23-MAY-1996; 96US-0652842.
 PR 23-NOV-1993; 93US-0156358.
 PR 12-AUG-1994; 94US-0289667.
 PR 23-MAY-1995; 95US-0447398.
 PR 31-OCT-1995; 95US-0551149.
 PR 06-DEC-1996; 96US-0568357.
 PR 21-SEP-1998; 98US-0157689.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Horwitz MA, Harth G;
 XX
 DR WPI; 2003-174073/17.
 DR N-PSDB; ABX75988.

XX New vaccine, useful for promoting an immune response against infectious
 PT pathogens of the genus Mycobacterium in a mammalian host -
 XX
 PS Example 1; Page 14-15; 82pp; English.

XX The invention describes a vaccine for promoting an immune response, in
 CC a mammalian host, against infectious pathogens of the genus
 CC Mycobacterium, comprising at least 1 immunodominant epitope of at least
 CC one majority abundant extracellular product comprising Mycobacterium
 CC tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14,
 CC 12 KD proteins or their analogues, homologues or subunits.
 CC The proteins and polypeptides of the invention are useful in gene
 CC therapy and treatment of diseases caused by Mycobacterium such as
 CC tuberculosis. This is the amino acid sequence of the Mycobacterium
 CC tuberculosis 30kDa protein.

XX SQ Sequence 325 AA;
 Query Match 100.0%; Score 1745; DB 24; Length 325;
 Best Local Similarity 100.0%; Pred. No. 1.2e-143;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFRRPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFRRPGLPVEYLQVPSMGR 60
 QY 61 DIKVOFSGGNNSPAVLLDGLRAODDYGNDINTPAFEWYQSLGSLVMPVGGSSFFS 120
 DB 61 DIKVOFSGGNNSPAVLLDGLRAODDYGNDINTPAFEWYQSLGSLVMPVGGSSFFS 120
 QY 121 DWSPACGKAGCQYKWTETLTSELPOWLSANRAVKPTGSAIIGLSMAGSSAMILAAVHP 180
 DB 121 DWSPACGKAGCQYKWTETLTSELPOWLSANRAVKPTGSAIIGLSMAGSSAMILAAVHP 180
 QY 181 QQFIYAGSLSALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPTQOIPL 240
 DB 181 QQFIYAGSLSALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPTQOIPL 240
 QY 241 VANNTRLWVYCGNGTPELNGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVFPPNG 300
 DB 241 VANNTRLWVYCGNGTPELNGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVFPPNG 300
 QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
 DB 301 THSWEYGAQLNAMKGDLOSSLGAG 325

RESULT 9
 ABB73461
 ID ABB73461 standard; Protein; 323 AA.
 AC ABB73461;
 XX
 DT 08-APR-2002 (first entry)
 XX
 DE M bovis 85B protein SEQ ID NO: 35.
 XX
 KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
 KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
 XX Th2 immune response; immunomodulatory.
 OS Mycobacterium bovis.
 XX
 PN US6328978-B1.
 XX
 PD 11-DEC-2001.
 XX
 PF 02-JUN-1999; 99US-0324542.
 XX
 PR 23-DEC-1997; 97US-0997080.
 XX

(GENE-) GENESIS RES & DEV CORP LTD.
 Watson JD, Tan PLJ, Prestidge R;
 WPI; 2002-138361/18.
 Inhibiting skin inflammation associated with skin disorder e.g. psoriasis, by administering composition comprising delipidated and deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae culture filtrate
 Example 5; Column 65-66; 116pp; English.
 The present invention relates to a method of inhibiting skin inflammation associated with a skin disorder selected from psoriasis, atopic dermatitis and allergic contact dermatitis, which involves administering a composition containing delipidated and deglycolipidated Mycobacterium vaccae cells or M. vaccae culture filtrate. The skin disorder to be treated may also include alopecia areata, and skin cancers such as basal cell carcinoma, squamous cell carcinoma and melanoma. The composition acts by inhibiting the Th2 immune response. The present invention is a protein described in the exemplification of the invention.
 SQ Sequence 323 AA;
 Query Match 97.8%; Score 1706; DB 23; Length 323;
 Best Local Similarity 98.5%; Pred. No. 3e-140;
 Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
 QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEMYQSGLSIVMPVGGSSFFYS 120
 DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEMYQSGLSIVMPVGGSSFFYS 120
 QY 121 DWSPACGKAGCQTYKWTFTLSELPGWLSANRAVKPTGSAALGLSWAGSSAMILAAAYHP 180
 DB 121 DWSPACGKAGCQTYKWTFTLSELPGWLSANRAVKPTGSAALGLSWAGSSAMILAAAYHP 180
 QY 181 QQFIYAGSLALLDPSQGMGLIGLAMDAGGYKAADMWGPSSDPWERNNDPTQIIPKL 240
 DB 181 QQFIYAGSLALLDPSQGMGLIGLAMDAGGYKAADMWGPSSDPWERNNDPTQIIPKL 238
 QY 241 VANNTRLWVYCGNGTPELGGANIPAEFLNFVRSSNLKFDAYNAAGGHNAVFNPFG 300
 DB 239 VANNTRLWVYCGNGTPELGGANIPAEFLNFVRSSNLKFDAYNAAGGHNAVFNPFG 298
 QY 301 THSWEYWGAGLNAKGDLSLQSLGAG 325
 DB 299 THSWEYWGAGLNAKGDLSLQSLGAG 323
 RESULT 10
 AA014855
 ID AA014855 standard; protein; 323 AA.
 AC AA014855;
 DX 25-OCT-1999 (first entry)
 XX Antigen 85B protein from M. bovis.
 XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 XX squamous cell carcinoma; melanoma.
 OS Mycobacterium bovis.
 XX

PN WO9932634-A2.
 XX PD 01-JUL-1999.
 XX PF 23-DEC-1998; 98WO-NZ00189.
 XX PR 04-DEC-1998; 98US-0205426.
 PR 23-DEC-1997; 97US-0996624.
 PR 23-DEC-1997; 97US-0997080.
 PR 23-DEC-1997; 97US-0997362.
 PR 11-JUN-1998; 98US-0095855.
 PR 17-SEP-1998; 98US-0156181.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
 WPI; 1999-430163/36.
 XX Enhancing immune response to an antigen
 XX Example 11; Page 158-159; 243pp; English.
 CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
 CC T cells and natural killer cells, to stimulate the production of
 CC cytokines, to enhance the expression of co-stimulatory molecules on
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation
 CC and function. The proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the proteins or
 CC nucleic acid sequences encoding the proteins can be used for the
 CC treatment, prevention, and detection of disorders including infectious
 CC diseases, immune disorders and cancer. In particular, the compounds and
 CC methods are used for treatment of diseases of the respiratory system,
 CC such as mycobacterial infections, asthma, allergies, tuberculosis,
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma.
 XX SQ Sequence 323 AA;
 Query Match 97.4%; Score 1699; DB 20; Length 323;
 Best Local Similarity 98.2%; Pred. No. 1.2e-139;
 Matches 319; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
 QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
 DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEMYQSGLSIVMPVGGSSFFYS 120
 DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEMYQSGLSIVMPVGGSSFFYS 120
 QY 121 DWSPACGKAGCQTYKWTFTLSELPGWLSANRAVKPTGSAALGLSWAGSSAMILAAAYHP 180
 DB 121 DWSPACGKAGCQTYKWTFTLSELPGWLSANRAVKPTGSAALGLSWAGSSAMILAAAYHP 180
 QY 181 QQFIYAGSLALLDPSQGMGLIGLAMDAGGYKAADMWGPSSDPWERNNDPTQIIPKL 240
 DB 181 QQFIYAGSLALLDPSQGMGLIGLAMDAGGYKAADMWGPSSDPWERNNDPTQIIPKL 238
 QY 241 VANNTRLWVYCGNGTPELGGANIPAEFLNFVRSSNLKFDAYNAAGGHNAVFNPFG 300
 DB 239 VANNTRLWVYCGNGTPELGGANIPAEFLNFVRSSNLKFDAYNAAGGHNAVFNPFG 298
 QY 301 THSWEYWGAGLNAKGDLSLQSLGAG 325
 DB 299 THSWEYWGAGLNAKGDLSLQSLGAG 323
 RESULT 11
 AA010486

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ID  AAR10486 standard; Protein; 325 AA.
XX  AAR10486;
AC  15-APR-1991 (first entry)
XX  DT
XX  Tuberculin active protein alpha-antigen.
XX  DE
XX  pneumonia; lung cancer; BCG live vaccine; tuberculin.
XX  KW
XX  Mycobacterium kansasii.
XX  OS
XX  Key Location/Qualifiers
XX  Peptide 1..40
XX  /label= signal peptide
XX  FT
XX  Protein 41..325
XX  /label= Tuberculin active protein alpha-antigen
XX  JP02308793-A.
XX  EN
XX  21-DEC-1990.
XX  PD
XX  22-MAY-1989; 89JP-0128091.
XX  PF
XX  22-MAY-1989; 89JP-0128091.
XX  PR
XX  (AJIN ) AJINOMOTO KK.
XX  PA
XX  WPI; 1991-041063/06.
XX  DR
XX  N-PSDB; AAQ10372.
XX  DT
XX  Alpha antigen derived from mycobacterium kansasii - for diagnosis
XX  PT of mycobacterium kansasii from pneumonia and lung cancer and for
XX  PT development of BCG vaccine
XX  PS
XX  Claim 1; Page 1; 11pp; Japanese.
XX  CC
XX  Alpha-antigen is produced in large quantities by culturing, under
XX  CC aerobic conditions, host cells that have been transformed with
XX  CC recombinant DNA comprising the sequence encoding the mature alpha-
XX  CC antigen and its signal sequence. The protein distinguishes
XX  CC M.kansasii disease from pneumonia or lung cancer.
XX  CC
XX  SQ Sequence 325 AA;
Query Match 91.8%; Score 1602; DB 12; Length 325;
Best Local Similarity 89.5%; Pred. No. 3.4e-131;
Matches 290; Conservative 20; Mismatches 14; Indels 0; Gaps 0;
QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
DB 1 MTDVSGKIRAWGRRLLVGAAAAAALPGLVGLAGGAATAGAFSRPGLPVEYHQPVAAMGR 60
QY 61 DIKVOFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
DB 61 SKVQFQSGGDNPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTFTLSELPMLSANRVPKPTGSAAGTSMAGSSAMILAAVHP 180
DB 121 DWYSPACGKAGCQTYKWTFTLSELPMLSANRVPKPTGSAAGTSMAGSSAMILAAVHP 180
QY 181 QOPIYAGSLSALDPSQGMPSLIGLAMDAGGYKAADMWGPSSDPAMERNPTQOIPKL 240
DB 181 QOPIYAGSLSALDPSQGMPSLIGLAMDAGGYKAADMWGPSSDPAMERNPTQOIPKL 240
QY 241 VANNTLWYCCNGTPELGGANIPAEFLNFRSSNLKFDQAYNAAGHNVAFFPNPG 300
DB 241 VANNTLWYCCNGTPELGGANIPAEFLNFRSSNLKFDQAYNAAGHNVAFFPNPG 300
QY 301 THSWEYWGACLNAKMGDLOSLGA 324
DB 301 THSWEYWGACLNAKMGDLOSLGA 324

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RESULT 12
AAR08099
ID  AAR08099 standard; protein; 325 AA.
XX  AAR08099;
AC  01-MAR-1991 (first entry)
XX  DT
XX  Mycobacterium derived alpha-antigen gene product.
XX  DE
XX  Vaccine; tuberculosis; HIV-1.
XX  KW
XX  Mycobacterium kansasii.
XX  OS
XX  Key Location/Qualifiers
XX  Peptide 1..40
XX  /label= Signal peptide
XX  FT
XX  Protein 41..325
XX  /label= Mature protein
XX  EP400973-A.
XX  EN
XX  05-DEC-1990.
XX  PD
XX  30-MAY-1990; 90EP-0305849.
XX  PF
XX  16-MAR-1990; 90JP-0064310.
XX  PR
XX  31-MAY-1989; 89JP-0135855.
XX  PA
XX  (AJIN ) AJINOMOTO KK.
XX  PI
XX  Matsuo K, Yamaguchi R, Yamazaki A, Yamada T;
XX  WPI; 1990-363461/49.
XX  DR
XX  N-PSDB; AAQ06668.
XX  DT
XX  New mycobacterial secretory vector - used to transform host
XX  PT cells, and vaccine comprising transformant
XX  CC
XX  Disclosure; Fig 1; 19pp; English.
XX  PS
XX  The signal peptide may be used to produce a recombinant protein
XX  CC comprising alpha-antigen and B-cell epitope of the HIV-1 gag
XX  CC antigen p17.
XX  CC The fused product is useful in vaccine production eg. tuberculosis.
XX  CC A live vaccine such as M.bovis BCG or M.smegmatis has a low toxicity
XX  CC and long lasting activity.
XX  CC
XX  SQ Sequence 325 AA;
Query Match 91.4%; Score 1595; DB 11; Length 325;
Best Local Similarity 89.2%; Pred. No. 1.4e-130;
Matches 289; Conservative 20; Mismatches 15; Indels 0; Gaps 0;
QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
DB 1 MTDVSGKIRAWGRRLLVGAAAAAALPGLVGLAGGAATAGAFSRPGLPVEYLQVPSAAMGR 60
QY 61 DIKVOFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
DB 61 SKVQFQSGGDNPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTFTLSELPMLSANRVPKPTGSAAGTSMAGSSAMILAAVHP 180
DB 121 DWYSPACGKAGCQTYKWTFTLSELPMLSANRVPKPTGSAAGTSMAGSSAMILAAVHP 180
QY 181 QOPIYAGSLSALDPSQGMPSLIGLAMDAGGYKAADMWGPSSDPAMERNPTQOIPKL 240
DB 181 QOPIYAGSLSALDPSQGMPSLIGLAMDAGGYKAADMWGPSSDPAMERNPTQOIPKL 240
QY 241 VANNTLWYCCNGTPELGGANIPAEFLNFRSSNLKFDQAYNAAGHNVAFFPNPG 300
DB 241 VANNTLWYCCNGTPELGGANIPAEFLNFRSSNLKFDQAYNAAGHNVAFFPNPG 300

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Db	241	VANTRTLWYCGNGTPELGGANVPAEFLENFVRSSNLKFDAYNAAGGHNAVFNLIDANG	300
QY	301	THSWEYGAQLNAMKGDLOSLGA	324
Db	301	THSWEYGAQLNAMKGDLOSLGA	324
RESULT 13			
AAW72943			
ID	AAW72943	standard; Protein; 403 AA.	
XX	AAW72943;		
XX	21-JAN-1999	(first entry)	
XX	Mycobacterium tuberculosis antigen ESAT6-MPT59.		
XX	Mycobacterium tuberculosis; antigen; vaccine; immunological;		
XX	immunogen; infection.		
XX	Mycobacterium tuberculosis.		
XX	W09844119-A1.		
XX	08-OCT-1998.		
XX	01-APR-1998;	98WO-DK00132.	
XX	05-JAN-1998;	98US-0070488.	
XX	02-APR-1997;	97DK-0000376.	
XX	18-APR-1997;	97US-0044624.	
XX	10-NOV-1997;	97DK-0001277.	
XX	(STAT-) STATENS SERUM INST.		
XX	Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB;		
XX	Rosenkrands I, Weidinger K;		
XX	WPI; 1998-542705/46.		
XX	New isolated mycobacteria polypeptides and nucleic acids - used for		
XX	developing products for the diagnosis of and vaccination against		
XX	mycobacterial infections, particularly tuberculosis		
XX	Disclosure; Page 233-234; 163pp; English.		
XX	The present sequence represents a Mycobacterium tuberculosis protein.		
XX	Products from the present invention, which describes protein fragments		
XX	and nucleic acid fragments derived from M. tuberculosis, can be used in		
XX	the detection of and prevention of mycobacterial infections. In		
XX	particular, the proteins and nucleic acids can be used for the diagnosis		
XX	of or vaccination against tuberculosis caused by M. tuberculosis,		
XX	M. africanum or M. bovis.		
SQ	Sequence	403 AA;	
Query Match	88.8%;	Score 1550;	DB 19; Length 403;
Best Local Similarity	99.3%;	Pred. No. 1.5e-126;	
Matches	286;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
QY	38	AGAFSRPGLFVEYLQVPSFSGMRDVKVQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA	97
Db	116	AKLFSRPLFVEYLQVPSFSGMRDVKVQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA	175
QY	98	FEWYQSGLSIVMPVGGQSFYSYSDWYSPACGAGCQTKWEFTLSELQWL SANRAVKP	157
Db	176	FEWYQSGLSIVMPVGGQSFYSYSDWYSPACGAGCQTKWEFTLSELQWL SANRAVKP	235
QY	158	TGSAIGLSWAGGSAMILAAHYHQFIYAGSLIALLDPQSGMPSLIGLAWGDAGYKAA	217
Db	236	TGSAIGLSWAGGSAMILAAHYHQFIYAGSLIALLDPQSGMPSLIGLAWGDAGYKAA	295
QY	218	DMWGFSSDPAWERNPTQIIPKLVANTRTLWYCGNGTPELGGANVPAEFLENFVRSSN	277
Db	296	DMWGFSSDPAWERNPTQIIPKLVANTRTLWYCGNGTPELGGANVPAEFLENFVRSSN	355
QY	278	LKFDAYNAAGGHNAVFNPNGTHSWEYGAQLNAMKGDLOSLGAG	325
Db	356	LKFDAYNAAGGHNAVFNPNGTHSWEYGAQLNAMKGDLOSLGAG	403
RESULT 14			
AAW21963			
ID	AAW21963	standard; Protein; 403 AA.	
XX	AAW21963;		
XX	06-SEP-1999	(first entry)	
XX	Amino acid sequence of antigen ESAT-6.		
XX	Immunogenic; Mycobacterium tuberculosis; immune response; infection;		
XX	tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;		
XX	pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;		
XX	CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;		
XX	CFP25A; CFP30B; CFP7B.		
XX	Mycobacterium tuberculosis.		
XX	W09924577-A1.		
XX	20-MAY-1999.		
XX	08-OCT-1998;	98WO-DK00438.	
XX	01-APR-1998;	98WO-DK00132.	
XX	10-NOV-1997;	97DK-0001277.	
XX	05-JAN-1998;	98US-0070488.	
XX	(STAT-) STATENS SERUM INST.		
XX	Andersen P, Skjot R;		
XX	WPI; 1999-347282/29.		
XX	New immunogenic fragment of Mycobacterium tuberculosis		
XX	Examples; Page 250-251; 265pp; English.		
XX	The invention describes a substantially pure immunogenic polypeptide		
XX	fragment (I) from Mycobacterium tuberculosis that is able to evoke a		
XX	protective immune response against infections by mycobacteria belonging		
XX	to the tuberculosis complex. The invention provides a (1) fusion		
XX	polypeptide comprising at least one polypeptide fragment (I) and at least		
XX	one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell		
XX	epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second		
XX	different amino acid sequence from M. tuberculosis, and/or including a		
XX	sequence which protects the first amino acid sequence from in vivo		
XX	degradation or post-translational processing; (3) a nucleic acid fragment		
XX	that encodes the above polypeptides. The polypeptides and nucleic acid		
XX	are useful as pharmaceuticals, for diagnosis of and as antigens for		
XX	vaccination against TB caused by Mycobacterium tuberculosis, africanum or		
XX	bovis. The polypeptides are also useful for diagnosing ongoing or		
XX	previous sensitization in an animal with bacteria belonging to the		
XX	tuberculosis complex. The invention also describes the use of CFP7A or		
XX	CFP30A or a T-cell epitope of for the induction of a strong immune		
XX	response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell		
XX	epitope of for diagnosis of TB in a mammal by performing a DTH type skin		
XX	test; use of CFP27, CFP30A, RD1-ORF3, RD1-ORF5, MPT59-ESAT6,		
XX	ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-		
XX	cell epitope of for the preparation of an immunological composition; and		
XX	for the preparation of a subunit vaccine.		
SQ	Sequence	403 AA;	
Query Match	88.8%;	Score 1550;	DB 20; Length 403;

Best Local Similarity 99.3%; Pred. No. 1.5e-126;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 AGAFSREGLPVEYLQVPSMGREDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 97
Db 116 AKLFSPREGLPVEYLQVPSMGREDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 175

QY 98 FEWYQSGLSIWMVPGQSSFYSDWYSPACGKAGCOTYKWEFTLTSELPOWLSANRAVKP 157
Db 176 FEWYQSGLSIWMVPGQSSFYSDWYSPACGKAGCOTYKWEFTLTSELPOWLSANRAVKP 235

QY 158 TGSAAIGLSWAGSSAMILAAHYHPOQFIYAGSLALLDPQSGMGPSLIGLAMGDAGGYKAA 217
Db 236 TGSAAIGLSWAGSSAMILAAHYHPOQFIYAGSLALLDPQSGMGPSLIGLAMGDAGGYKAA 295

QY 218 DMWGPSSDPAWERNPTQIQIPKLVANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSN 277
Db 296 DMWGPSSDPAWERNPTQIQIPKLVANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSN 355

QY 278 LKFDAYNAAGGHNAVFNPNGTHSWYWGAGLQNAKMGDLQSSLGAG 325
Db 356 LKFDAYNAAGGHNAVFNPNGTHSWYWGAGLQNAKMGDLQSSLGAG 403

RESULT 15
AAW72942
ID AAW72942 standard; Protein; 404 AA.
XX AC AAW72942;
XX DT 21-JAN-1999 (first entry)
XX DE Mycobacterium tuberculosis antigen MPT59-ESAT6.
XX KW Mycobacterium tuberculosis; antigen; vaccine; immunological;
XX KW immunogen; infection.
XX OS Mycobacterium tuberculosis.
XX PN WO9844119-A1.
XX PD 08-OCT-1998.
XX PF 01-APR-1998; 98WO-DK00132.
XX PR 05-JAN-1998; 98US-0070488.
XX PR 02-APR-1997; 97DK-0000376.
XX PR 18-APR-1997; 97US-0044624.
XX PR 10-NOV-1997; 97DK-0001277.
XX (STAT-) STATENS SERUM INST.
XX Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB;
XX Rosenkrands I, Wieding K;
XX WPI; 1998-542705/46.
XX New isolated mycobacteria polypeptides and nucleic acids - used for
XX developing products for the diagnosis of or vaccination against
XX mycobacterial infections, particularly tuberculosis
XX Disclosure; page 232-233; 163pp; English.
XX The present sequence represents a Mycobacterium tuberculosis protein.
XX Products from the present invention, which describes protein fragments
XX and nucleic acid fragments derived from M. tuberculosis, can be used in
XX the detection of and prevention of mycobacterial infections. In
XX particular, the proteins and nucleic acids can be used for the diagnosis
XX of or vaccination against tuberculosis caused by M. tuberculosis,
XX M. africanum or M. bovis.
XX Sequence 404 AA;
SQ

Query Match 88.8%; Score 1550; DB 19; Length 404;
Best Local Similarity 99.7%; Pred. No. 1.5e-126;
Matches 285; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 40 AFSPRGLPVEYLQVPSMGREDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 99
Db 21 SFSPRGLPVEYLQVPSMGREDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 80

QY 100 WYQSGLSIWMVPGQSSFYSDWYSPACGKAGCOTYKWEFTLTSELPOWLSANRAVKPTG 159
Db 81 WYQSGLSIWMVPGQSSFYSDWYSPACGKAGCOTYKWEFTLTSELPOWLSANRAVKPTG 140

QY 160 SAAIGLSWAGSSAMILAAHYHPOQFIYAGSLALLDPQSGMGPSLIGLAMGDAGGYKAA 219
Db 141 SAAIGLSWAGSSAMILAAHYHPOQFIYAGSLALLDPQSGMGPSLIGLAMGDAGGYKAA 200

QY 220 WGPSSDPAWERNPTQIQIPKLVANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLK 279
Db 201 WGPSSDPAWERNPTQIQIPKLVANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLK 260

QY 280 FQDAYNAAGGHNAVFNPNGTHSWYWGAGLQNAKMGDLQSSLGAG 325
Db 261 FQDAYNAAGGHNAVFNPNGTHSWYWGAGLQNAKMGDLQSSLGAG 306

RESULT 16
AAAY21962
ID AAAY21962 standard; Protein; 404 AA.
XX AC AAAY21962;
XX DT 06-SEP-1999 (first entry)
XX DE Amino acid sequence of antigen MPT59.
XX KW Immunogenic; Mycobacterium tuberculosis; immune response; infection;
XX KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
XX KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
XX KW CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
XX KW CFP25A; CFP30B; CFP7B.
XX OS Mycobacterium tuberculosis.
XX PN WO9924577-A1.
XX PD 20-MAY-1999.
XX PF 08-OCT-1998; 98WO-DK00438.
XX PR 01-APR-1998; 98WO-DK00132.
XX PR 10-NOV-1997; 97DK-0001277.
XX PR 05-JAN-1998; 98US-0070488.
XX (STAT-) STATENS SERUM INST.
XX Andersen P, Skjot R;
XX WPI; 1999-347282/29.
XX New immunogenic fragment of Mycobacterium tuberculosis
XX Examples; page 249-250; 265pp; English.
XX The invention describes a substantially pure immunogenic polypeptide
XX fragment (1) from Mycobacterium tuberculosis that is able to evoke a
XX protective immune response against infections by mycobacteria belonging
XX to the tuberculosis complex. The invention provides a (1) fusion
XX polypeptide comprising at least one polypeptide fragment (1) and at least
XX one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
XX epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
XX different amino acid sequence from M. tuberculosis, and/or including a
XX sequence which protects the first amino acid sequence from in vivo
XX degradation or post-translational processing; (3) a nucleic acid fragment

that encodes the above polypeptides. The polypeptides and nucleic acid are useful as pharmaceuticals, for diagnosis of and as antigens for vaccination against TB caused by *Mycobacterium tuberculosis*, *M. bovis*. The polypeptides are also useful for diagnosing ongoing or previous sensitization in an animal with bacteria belonging to the tuberculosis complex. The invention also describes the use of CFP7A or CFP30A or a T-cell epitope for the induction of a strong immune response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell epitope for diagnosis of TB in a mammal by performing a DTH type skin test; use of CFP27, CFP30A, RDI-ORF2, RDI-ORF3, MPT59-ESAT6, ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-cell epitope for the preparation of an immunological composition; and for the preparation of a subunit vaccine.

Query Match	88.8%;	Score 1550;	DB 20;	Length 404;
Best Local Similarity	99.7%;	Pred. No. 1.5e-126;		
Matches 285; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	40	AFSRPGLPVBYLQVPSFSGMRD	IKVQCSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE	99
Db	21	SFSRPLPVBYLQVPSFSGMRD	IKVQCSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE	80
QY	100	WYQSGLSIWMVGGQSSFFSDWYSPACGKAGCCTYKWEFTLTSELQWL	SANRAVPRTG	159
Db	81	WYQSGLSIWMVGGQSSFFSDWYSPACGKAGCCTYKWEFTLTSELQWL	SANRAVPRTG	140
QY	160	SAAIGL\$MAGSSAMILAAHYHPQOFIYAGLSALIDPSQGMGPSLILGLAMGDAGGYKAA	DM	219
Db	141	SAAIGL\$MAGSSAMILAAHYHPQOFIYAGLSALIDPSQGMGPSLILGLAMGDAGGYKAA	DM	200
QY	220	WGPSSDPAMERNPTQOI PKLVANNTRLWYCGNGTNELGGANI PAEFLNFVRSSNLK		279
Db	201	WGPSSDPAMERNPTQOI PKLVANNTRLWYCGNGTNELGGANI PAEFLNFVRSSNLK		260
QY	280	FODAYNAAGGHNAVFNPNGNTHSWEYWGQALNAMKGDLOSSTIGAG		325
Db	261	FQDAYNAAGGHNAVFNPNGNTHSWEYWGQALNAMKGDLOSSTIGAG		306

XX	Claim 11; Fig 19; 105pp; English.
PS	The present sequence represents the alpha antigen of Mycobacterium
CC	avium. The alpha antigen is an abundantly produced, secreted 30
CC	kilodalton mycobacterial protein involved in mycolic acid synthesis. It
CC	is an useful indicator of mycobacterial disease as it can account for up
CC	to 20% of the protein content of spent mycobacterial culture medium. In
CC	addition, homologous alpha proteins exist for most species of
CC	Mycobacteria. Monoclonal antibodies were produced against the present
CC	sequence and its fragments. These can be used for the detection of
CC	Mycobacteria in a test sample. The method can be used for the detection
CC	of Mycobacteria such as M. tuberculosis, M. avium and M. intracellulare.
CC	The method can be used to monitor the progression of therapy in
CC	individuals infected with Mycobacteria.
XX	
SQ	Sequence 330 AA;
Query Match	87.2%; Score 1522; DB 19; Length 330;
Best Local Similarity	84.9%; Pred. No. 3.3e-124;
Matches 275; Conservative 24; Mismatches 25; Indels 0; Gaps 0;	
Qy	1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVLGAGGAATAGFSPCLPVEYLQVPSPMGR 60
Db	1 MTDLSEKVRAWGRLLLVGAAAATVPLGLIAGGAATANASRPGIPVEYLQVPSSAGMR 60
Qy	61 DIKVQFSQGNNSPAIVLLDGLRAODDNGWDINTPAFEWYQSGLSTWMPVGQSSFPYS 120
Db	61 DIKVQFSQGGNSPAVLLDGLRAODDNGWDINTPAFEWYQSGLSVIMPVGQSSFFA 120
Qy	121 DWYSPACGKAGCQTWKETFTLTSELPOWLISANRAVKPTGSAAIGLSMAGSSAMITLAAVHP 180
Db	121 DWYQAPCGKAGCSTWKETFTLTSELPSYLIASNKGVRTGNAAGVLSMGSSAMITLVNHP 180
Qy	181 QOFTYAGSLISALLDSPSQGNPSLIGLAMGDAGGYKAADWMGFSSDPDAWERNDPTQQIPKL 240
Db	181 DOFTYAGSLISALLDSPSQGMPSLILGLAMGDAGGYKADAMWGFPSSDPDAQWRNDPSLIHPEL 240
Qy	241 VANNTRLMVYCNGTPNELGCANIPAELENFVRSSNLKFODAYNAGGHNAVFNFPNG 300
Db	241 VGHNTRLMVYCNGTPSELGGHANPEEFLENFVRSSNLKFODAYNGAGGHNAVFNFNANG 300
Qy	301 THSWEYGAQLNAMKGDLOSSLGA 324
Db	301 THSWEYGAQLNAMKPDLOGTLGA 324

RESULT 18	
AAP90109	
ID	AAP90109 standard; protein; 283 AA.
XX	
AC	AAP90109;
XX	
DT	01-NOV-1989 (first entry)
XX	
DE	Tuberculin active protein alpha-antigen.
XX	
KW	Tuberculin active protein alpha-antigen; Mycobacterium
KW	bovis; tuberculous cephalomeningitis.
XX	
OS	Mycobacterium bovis.
XX	
PN	JP01144994-A.
XX	
PD	07-JUN-1989.
XX	
PF	02-DEC-1987; 87JP-0305250.
XX	
PR	02-DEC-1987; 87JP-0305250.
XX	
PA	(AJIN) AJINOMOTO KK.
XX	
DR	WPI; 1989-209292/29.

DR N-PSDB; AAN90130.
XX Alpha-antigen derived from BCG bacteria - used for diagnosing
PT tuberculous cephalomeningitis.
XX
XX
PS Claim 1; page 576; pp; Japanese.
XX
XX Tuberculin active protein alpha-antigen is derived from Mycobacterium
CC bovis (see AAN90130). The protein is useful as a pharmaceutical agent
CC for diagnosing tuberculous cephalomeningitis.
XX
SQ Sequence 283 AA;

Query Match 86.5%; Score 1510; DB 10; Length 283;
Best Local Similarity 98.2%; Pred. No. 3e-123;
Matches 280; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 41 FSRGLPVEYLQVPSMGRDIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEW 100
Db 1 FSRGLPVEYLQVPSMGRDIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEW 60
QY 101 YYQSGLSIVMPVGQSSPYSDWYSPACGACQTYKWTFTLTSELPOWLSANRAVKPTGS 160
Db 61 YYQSGLSIVMPVGQSSPYSDWYSPACGACQTYKWTFTLTSELPOWLSANRAVKPTGS 120
QY 161 AAIGLSMAGSSAMILAAVHPOOFIYAGSLSALLDPSQGMG--LIGLAMGDAGGYKAADMW 220
Db 121 AAIGLSMAGSSAMILAAVHPOOFIYAGSLSALLDPSQGMG--LIGLAMGDAGGYKAADMW 178
QY 221 GPSSDPAPERNDPTQOIPKLVANNTLWYVCGNGTPNELGGANIPAEFLENFVRSSNLKF 280
Db 179 GPSSDPAPERNDPTQOIPKLVANNTLWYVCGNGTPNELGGANIPAEFLENFVRSSNLKF 238
QY 281 QDAYNAGGHNAVFNPFGTHGTHSWEYGAQLNAMKGDILQSSILGAG 325
Db 239 QDAYNAGGHNAVFNPFGTHGTHSWEYGAQLNAMKGDILQSSILGAG 283

RESULT 19
AAY14851
ID AAY14851 standard; protein; 327 AA.
XX
AC AAY14851;
XX
DT 25-OCT-1999 (first entry)
XX
DE Antigen 85B protein from M. leprae.
XX
KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma.
XX
OS Mycobacterium leprae.
XX
PN W09932634-A2.
XX
PD 01-JUL-1999.
XX
PF 23-DEC-1998; 98WO-NZ00189.
XX
PR 04-DEC-1998; 98US-0205426.
PR 23-DEC-1997; 97US-0996624.
PR 23-DEC-1997; 97US-0997080.
PR 23-DEC-1997; 97US-0997362.
PR 11-JUN-1998; 98US-0095855.
PR 17-SEP-1998; 98US-0156181.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
PI

XX WPI; 1999-430163/36.
DR
XX Enhancing immune response to an antigen
PT
XX
PS Example 11; Page 154-155; 243pp; English.
XX
XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
CC T cells and natural killer cells, to stimulate the production of
CC cytokines, to enhance the expression of co-stimulatory molecules on
CC dendritic cells and monocytes, and to enhance dendritic cell maturation
CC and function. The proteins can be expressed by standard recombinant
CC methodology. Pharmaceutical compositions comprising the proteins or
CC nucleic acid sequences encoding the proteins can be used for the
CC treatment, prevention, and detection of disorders including infectious
CC diseases, immune disorders and cancer. In particular, the compounds and
CC methods are used for treatment of diseases of the respiratory system,
CC such as mycobacterial infections, asthma, allergies, tuberculosis,
CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma.
SQ Sequence 327 AA;

Query Match 83.3%; Score 1454; DB 20; Length 327;
Best Local Similarity 83.0%; Pred. No. 2.7e-118;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MIDVSGKIRAWGRLLVG--AAATLPSLISLAGGAATAGAFSRPGLPVEYLQVPSMGR 58
QY 61 DIKVOFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSPYSDW 120
Db 59 TIKVQFQNGGSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGQSSPYSDW 118
QY 121 DWYSPACGACQTYKWTFTLTSELPOWLSANRAVKPTGSAAIGLSMAGSSAMILAAVH 180
Db 119 DWYSPACGACQTYKWTFTLTSELPOWLSANRAVKPTGSAAIGLSMAGSSAMILAAVH 178
QY 181 QQFIYAGSLSALLDPSQGMGPFSLIGLAMGDAGGYKAADMWGPSSDPAPERNDPTQOIPKL 240
Db 179 DQFIYAGSLSALLDPSQGMGPFSLIGLAMGDAGGYKAADMWGPSSDPAPERNDPTQOIPKL 238
QY 241 VANNTRLWYVCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNPFGTH 300
Db 239 VANNTRLWYVCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNPFGTH 298
QY 301 THSWEYGAQLNAMKGDILQSSILGA 324
Db 299 THSWEYGAQLNAMKGDILQSSILGA 322

RESULT 20
ABB73457
ID ABB73457 standard; Protein; 327 AA.
XX
AC ABB73457;
XX
DT 08-APR-2002 (first entry)
XX
DE M leprae 85B protein SEQ ID NO: 31.
XX
KW Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory.
XX
OS Mycobacterium leprae.
XX
PN US6328978-B1.

XX 11-DEC-2001.
 XX 02-JUN-1999; 99US-0324542.
 XX 23-DEC-1997; 97US-0997080.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 XX Watson JD, Tan PLJ, Prestidge R;
 XX WPI; 2002-138361/18.
 XX Inhibiting skin inflammation associated with skin disorder e.g.
 XX psoriasis, by administering composition comprising delipidated and
 XX deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
 XX culture filtrate -
 XX Example 5; Column 57-60; 116pp; English.
 XX The present invention relates to a method of inhibiting skin inflammation
 XX associated with a skin disorder selected from psoriasis, atopic
 XX dermatitis and allergic contact dermatitis, which involves administering
 XX a composition containing delipidated and deglycolipidated Mycobacterium
 XX vaccae cells or M. vaccae culture filtrate. The skin disorder to be
 XX treated may also include alopecia areata, and skin cancers such as basal
 XX cell carcinoma, squamous cell carcinoma and melanoma. The composition
 XX acts by inhibiting the Th2 immune response. The present sequence is a
 XX protein described in the exemplification of the invention.
 XX Sequence 327 AA;
 XX Query Match 83.3%; Score 1454; DB 23; Length 327;
 XX Best Local Similarity 83.0%; Pred. No. 2.7e-118;
 XX Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;
 QY 1 MTDVSRKIRAWGRMLTGTAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
 Db 1 MIDVSGKIRAWGRWLLVG--AAATLPSLLIAGGAATASAFSRPGLPVEYLQVPSMGR 58
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFWYQSGLSIVMPVGGQSFYS 120
 Db 59 TIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTSAFWYQSGLSIVMPVGGQSFYS 118
 QY 121 DWTSPPACGKAGCOTYKWEFTLTSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAAYHP 180
 Db 119 DWTSPPACGKAGCOTYKWEFTLTSELPOWLSANRAVKPTGSAATGLSMAGSSAMILAAAYHP 178
 QY 181 QQFIYAGLSALLDPQSGMGPSLIGLAWGAGGKADMGKPSDDPAWERNDDTQIIPKL 240
 Db 179 DQFIYAGLSALLDPQSGMGPSLIGLAWGAGGKADMGKPSDDPAWERNDDTQIIPKL 238
 QY 241 VANNTRILWVYCGNGTPELNGGNIIPAEFLFNFRSSNLKFDQAYNNAAGGHNVAFFNPNG 300
 Db 239 VANNTRILWVYCGNGTPELNGGNIIPAEFLFNFRSSNLKFDQAYNNAAGGHNVAFFNPNG 298
 QY 301 THSWEYWGALNNAKMGDLQSSLGA 324
 Db 299 THSWEYWGALNNAKMGDLQSSLGA 322
 RESULT 21
 ID ABB83662 standard; Protein; 285 AA.
 XX ABB83662;
 XX 15-NOV-2002 (first entry)
 XX Mycobacterium-originated alpha antigen.
 XX Antiallergic; Dermatological; Antiasthmatic; Antiinflammatory;
 XX Ophthalmological; Mycobacterium-originated alpha antigen;

KW allergic disease; atopic dermatitis; asthma; allergic rhinitis;
 KW allergic conjunctivitis; interleukin-4; Th2-type cytokine;
 XX Ige production; histamine; eosinophilic infiltration.
 OS Mycobacterium kansasii.
 FN WO200266055-A1.
 XX 29-AUG-2002.
 XX 20-FEB-2002; 2002WO-JP01459.
 XX 20-FEB-2001; 2001JP-0043291.
 PA (PRIM-) PRIMMUNE CORP INC.
 XX Yasutomi Y, Mizutani H;
 XX WPI; 2002-667038/71.
 XX Medicinal use of Mycobacterium-originated alpha-antigen or its gene in
 XX treating allergic diseases e.g. atopic dermatitis, asthma, allergic
 XX rhinitis and allergic conjunctivitis -
 XX Disclosure; Page 27-28; 34pp; Japanese.
 XX This invention relates to pharmaceutical compositions for preventing
 XX or treating allergic diseases containing Mycobacterium-originated
 XX alpha antigens. The compositions are antiallergic, dermatological,
 XX antiasthmatic, antiinflammatory and ophthalmological. The antigen and
 XX its encoded gene are for producing drug compositions in treating
 XX allergic diseases e.g. atopic dermatitis, asthma, allergic rhinitis
 XX and allergic conjunctivitis. The drug compositions are made from the
 XX protein that can inhibit production of interleukin-4, ameliorate
 XX Th2-type cytokine-predominate immune state and relieve
 XX symptoms of allergic diseases such as Ige production, histamine
 XX release and eosinophilic infiltration. The present sequence
 XX represents the mycobacterium-originated alpha antigen. This
 XX sequence is not encoded by the sequence featured in ABQ79295 despite
 XX being said to do so in the specification.
 XX Sequence 285 AA;

Query Match 82.3%; Score 1437; DB 23; Length 285;
 Best Local Similarity 90.5%; Pred. No. 6.8e-117;
 Matches 257; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
 QY 41 FSRPGLPVEYLQVPSMGRDIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFW 100
 Db 1 FSRPGLPVEYLQVPSMGRDIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFW 60
 QY 101 YQSGLSIVMPVGGQSFYSQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFW 160
 Db 61 YQSGLSIVMPVGGQSFYSQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFW 120
 QY 161 AATGLSMAGSSAMILAAAYHPQFIYAGLSALLDPQSGMGPSLIGLAWGAGGKADMG 220
 Db 121 AAVGISWAGSSALLSVYHPQFIYAGLSALLDPQSGMGPSLIGLAWGAGGKADMG 180
 QY 221 GPSSDPAWERNDDTQIIPKLVAANNTRILWVYCGNGTPELNGGNIIPAEFLFNFRSSNLKF 280
 Db 181 GPSSDPAWERNDDTQIIPKLVAANNTRILWVYCGNGTPELNGGNIIPAEFLFNFRSSNLKF 240
 QY 281 QDAYNNAAGGHNVAFFNPNGTHSWEYWGALNNAKMGDLQSSLGA 324
 Db 241 QDAYNNAAGGHNVAFFNPNGTHSWEYWGALNNAKMGDLQSSLGA 284

RESULT 22
 ABB83662
 ID ABB83662 standard; Protein; 337 AA.
 XX ABB83662;
 XX 15-NOV-2002 (first entry)
 XX Mycobacterium-originated alpha antigen.

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XX DT 31-MAR-2003 (first entry)
XX DE Mycobacterium tuberculosis 32kDa protein.
XX KW Antibacterial; tuberculosis; vaccine; gene therapy; 32kDa protein.
XX OS Mycobacterium tuberculosis.
XX PN US2002131975-A1.
XX PD 19-SEP-2002.
XX PF 14-SEP-2001; 2001US-0953510.
XX PR 23-MAY-1996; 96US-0652842.
XX PR 23-NOV-1993; 93US-0156358.
XX PR 12-AUG-1994; 94US-0289667.
XX PR 23-MAY-1995; 95US-0447398.
XX PR 31-OCT-1995; 95US-0551149.
XX PR 06-DEC-1996; 96US-0568357.
XX PR 21-SEP-1998; 98US-0157689.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Horwitz MA, Harth G;
XX DR WPI; 2003-174073/17.
XX DR N-PSDB; ABX75989.
XX PT New vaccine, useful for promoting an immune response against infectious
XX PT pathogens of the genus Mycobacterium in a mammalian host
XX PS Example 1; Page 15-16; 82pp; English.
XX CC The invention describes a vaccine for promoting an immune response, in
XX CC a mammalian host, against infectious pathogens of the genus
XX CC Mycobacterium, comprising at least 1 immunodominant epitope of at least
XX CC one majority abundant extracellular product comprising Mycobacterium
XX CC tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14,
XX CC 12 kD protein or their analogues, homologues or subunits.
XX CC The proteins and polypeptides of the invention are useful in gene
XX CC therapy and treatment of diseases caused by Mycobacterium such as
XX CC tuberculosis. This is the amino acid sequence of the Mycobacterium
XX CC tuberculosis 32kDa protein.
XX SQ Sequence 337 AA;
    Query Match      80.6%; Score 1407; DB 24; Length 337;
    Best Local Similarity 78.9%; Pred. No. 3.5e-114;
    Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
QY 8 IRWGRRLMIGTAAAVVFLVGLAGGAATAGAFSRPGLPVEYLQVPSPMGRDIKVQFQ 67
DB 11 VTGMSRRLLVVGGAALVSLGAVGTATAGAFSRPGLPVEYLQVPSPMGRDIKVQFQ 70
QY 68 SGGNSPAVLLDGLRAQDNYGNDINTPAFWYVQSGLSIVMPVGGQSSFYSDWYSAC 127
DB 71 SGGNSPALYLLDGLRAQDDPSGNDINTPAFEWDQSGLSVMPVGGQSSFYSDWYQAC 130
QY 128 GKAGQQTWETFLTSELPWLSANRAVKPTGSAAGLSMAGSSAMILAAYHPQOFIVAG 187
DB 131 GRAGQQTWETFLTSELPWLSANRAVKPTGSAAGLSMAGSSAMILAAYHPQOFIVAG 190
QY 188 SLUALDPSQGMGSPSLIGLAMGAGGYKAADWVGSPSSPAWRNPDQIQIPKLNVNREL 247
DB 191 AMSGLLDPSQGMGPTLIGLAMGAGGYKASDMWGPKEPDPAWQRNDPLLNVGKLIAINTRV 250
QY 248 WYVCGNCTNEIGGANIPAEFLNFVRSNLKFDAYNAAGCHNAVFNPNGTHSEWYV 307
DB 251 WYVCGNGKPSLDGNNLPAKFLGFEVFTSNIKFDAYNAAGGHHGVDFPDPSGTHSEWYV 310
QY 308 GAQLNAMKGLQSLGA 324
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Db 311 GAQLNAMKPDQLQALGA 327
RESULT 23
AAW18165
ID AAW18165 standard; Protein; 338 AA.
XX AC AAW18165;
XX DT 13-AUG-1997 (first entry)
XX DE Mycobacterium tuberculosis extracellular 32AKD protein.
XX KW Vaccine; vaccinating agent; M.tuberculosis; pathogen; bacteria;
XX OS virus; fungus; protozoan; HIV.
XX PF Mycobacterium tuberculosis.
XX FT Key Location/Qualifiers
XX FT Protein 44..338
XX FT /label= Mature
XX PN W09637219-A1.
XX PD 28-NOV-1996.
XX PF 23-MAY-1996; 96WO-US07781.
XX PR 06-DEC-1995; 95US-0568357.
XX PR 23-MAY-1995; 95US-0447398.
XX PR 20-OCT-1995; 95US-0545926.
XX PR 31-OCT-1995; 95US-0551149.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Harth G, Horwitz MA;
XX DR WPI; 1997-020936/02.
XX DR N-PSDB; AAT71599.
XX PT Vaccines derived from M.tuberculosis major abundant extracellular
XX PT proteins - are easy to prepare and less toxic than conventional
XX PT killed or attenuated vaccines, useful for protecting against or
XX PT treating Mycobacterial infections
XX PS Claim 1; Page 36-38; 193pp; English.
XX CC A vaccinating agent for promoting an immune response in a mammal
XX CC against Mycobacterium pathogens comprises at least one majorly abundant
XX CC extracellular protein, i.e. the M.tuberculosis 110, 80, 71, 58, 45,
XX CC 32A, 32B, 30, 24, 23.5, 23, 16, 14 or 12 kD proteins, or their
XX CC analogues, homologues and subunits. The present sequence represents the
XX CC 32A kD protein. The vaccinating agents are used to protect against (or
XX CC to treat existing) infections by Mycobacterium (especially M.
XX CC tuberculosis) while the epitopes can also be used to detect presence
XX CC of an immune response to a Mycobacterium pathogen. The vectors,
XX CC containing the DNA for the extracellular proteins, are used to transform
XX CC cells for production of recombinant DNA molecules. More generally the
XX CC DNA from other pathogens can be used in vaccines, e.g. against other
XX CC bacteria, viruses, fungi and protozoa. Since different combinations of
XX CC DNA can be used, a wide range of effective compositions can be produced.
XX CC They generate a response against the antigens most often found on
XX CC infected cells during the infection, regardless of the strength or
XX CC specificity of the immune response. The vaccines are easy to produce
XX CC and less toxic than known killed or attenuated vaccines, so can be given
XX CC to immunocompromised subjects, e.g. those with HIV infection.
XX SQ Sequence 338 AA;
    Query Match      80.6%; Score 1407; DB 18; Length 338;
    Best Local Similarity 78.9%; Pred. No. 3.5e-114;
    Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
```


XX PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
XX DR WPI; 1999-430163/36.
XX PT Enhancing immune response to an antigen
XX PS Example 11; Page 155-156; 243pp; English.
XX XX The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
CC T cells and natural killer cells, to stimulate the production of
CC cytokines, to enhance the expression of co-stimulatory molecules on
CC dendritic cells and monocytes, and to enhance dendritic cell maturation
CC and function. The proteins can be expressed by standard recombinant
CC methodology. Pharmaceutical compositions comprising the proteins or
CC nucleic acid sequences encoding the proteins can be used for the
CC treatment, prevention, and detection of disorders including infectious
CC diseases, immune disorders and cancer. In particular, the compounds and
CC methods are used for treatment of diseases of the respiratory system,
CC such as mycobacterial infections, asthma, allergies, tuberculosis,
CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma.
XX SQ Sequence 338 AA;
Query Match 80.6%; Score 1407; DB 20; Length 338;
Best Local Similarity 78.9%; Pred. No. 3.5e-114;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
QY 8 IRWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGRDIKVQFQ 67
Db 11 VTGMSRLVVGAAGAAVGLVGVGAVGTATAGAFSRPGLPVEYLQVPSMGRDIKVQFQ 70
QY 68 SGGNSPAILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSDWYSPAC 127
Db 71 SGANSALYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSDWYQFAC 130
QY 128 GKAGCQTYKWEFTLSELFWLSANRAVKPTGSAIGLSMAGSSAMILAAYHPQFIYAG 187
Db 131 GKAGCQTYKWEFTLSELFWLSANRAVKPTGSAIGLSMAGSSAMILAAYHPQFVIYAG 190
QY 188 SILSALLDPQGMGSPSLIGLAMGDAGYKAADMMWGPSSDPANERNPTQOIPKLVANTRL 247
Db 191 AMSGLLDPSQAMGPTLIGLAMGDAGYKASDMWGPKEPDAWQRNDPDLNVLNTRV 250
QY 248 WYTCNGTNPNEGNIPIAEFLNFVRSSNLKFDQAYNAGGHNAPFNPNTHSWEYW 307
Db 251 WYTCNGKTPSDLGNNLPKLFEGFVRTSNIKFDQAYNAGGHNAPFNPNTHSWEYW 310
QY 308 GAQLNAMKGDLOSSLGA 324
Db 311 GAQLNAMKPDQLRALGA 327
RESULT 26
AA14854
ID AA14854 standard; protein; 338 AA.
XX AC AA14854;
XX DT 25-OCT-1999 (first entry)
XX DE Antigen 85A protein from M. bovis.
XX XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma.

XX OS Mycobacterium bovis.
XX PN WO9932634-A2.
XX XX 01-JUL-1999.
XX PF 23-DEC-1998; 98WO-NZ00189.
XX PR 04-DEC-1998; 98US-0205426.
XX PR 23-DEC-1997; 97US-0996624.
XX PR 23-DEC-1997; 97US-0997080.
XX PR 23-DEC-1997; 97US-0997362.
XX PR 11-JUN-1998; 98US-0095855.
XX PR 17-SEP-1998; 98US-0156181.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX PA Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;
XX PI WPI; 1999-430163/36.
XX DR Enhancing immune response to an antigen
XX PT Example 11; Page 157-158; 243pp; English.
XX PS The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
CC T cells and natural killer cells, to stimulate the production of
CC cytokines, to enhance the expression of co-stimulatory molecules on
CC dendritic cells and monocytes, and to enhance dendritic cell maturation
CC and function. The proteins can be expressed by standard recombinant
CC methodology. Pharmaceutical compositions comprising the proteins or
CC nucleic acid sequences encoding the proteins can be used for the
CC treatment, prevention, and detection of disorders including infectious
CC diseases, immune disorders and cancer. In particular, the compounds and
CC methods are used for treatment of diseases of the respiratory system,
CC such as mycobacterial infections, asthma, allergies, tuberculosis,
CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma.
XX SQ Sequence 338 AA;
Query Match 80.6%; Score 1407; DB 20; Length 338;
Best Local Similarity 78.9%; Pred. No. 3.5e-114;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
QY 8 IRWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGRDIKVQFQ 67
Db 11 VTGMSRLVVGAAGAAVGLVGVGAVGTATAGAFSRPGLPVEYLQVPSMGRDIKVQFQ 70
QY 68 SGGNSPAILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSDWYSPAC 127
Db 71 SGANSALYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSDWYQFAC 130
QY 128 GKAGCQTYKWEFTLSELFWLSANRAVKPTGSAIGLSMAGSSAMILAAYHPQFIYAG 187
Db 131 GKAGCQTYKWEFTLSELFWLSANRAVKPTGSAIGLSMAGSSAMILAAYHPQFVIYAG 190
QY 188 SILSALLDPQGMGSPSLIGLAMGDAGYKAADMMWGPSSDPANERNPTQOIPKLVANTRL 247
Db 191 AMSGLLDPSQAMGPTLIGLAMGDAGYKASDMWGPKEPDAWQRNDPDLNVLNTRV 250
QY 248 WYTCNGTNPNEGNIPIAEFLNFVRSSNLKFDQAYNAGGHNAPFNPNTHSWEYW 307
Db 251 WYTCNGKTPSDLGNNLPKLFEGFVRTSNIKFDQAYNAGGHNAPFNPNTHSWEYW 310
QY 308 GAQLNAMKGDLOSSLGA 324
Db 311 GAQLNAMKPDQLRALGA 327

QY	128	GKAGCQTYKWTETFLTITSELP	OWLSANRAVKPTGSAATGLS	MAGSSAMILAAHYHPOQFIYAG	187
Db	131	GKAGCQTYKWTETFLTITSELP <th>QWLOANRHVKTGSAVVGLS</th> <th>MAASSALTALYHPQQFVYAG</th> <th>190</th>	QWLOANRHVKTGSAVVGLS	MAASSALTALYHPQQFVYAG	190
QY	188	SLSALLDPSQMGPSLIGLAMGD <th>AGYKAADMMGPSSDP</th> <th>PAWERNDPTQOIPKLVANNTSL</th> <th>247</th>	AGYKAADMMGPSSDP	PAWERNDPTQOIPKLVANNTSL	247
Db	191	AMSGLLDPSQAMGPTLIGLAMG <th>DAGYKASDMMGPKED</th> <th>PAWQRNDPLLVNGLIANNTRV</th> <th>250</th>	DAGYKASDMMGPKED	PAWQRNDPLLVNGLIANNTRV	250
QY	248	WVYCGNGTPELGGANIPAEFL <th>ENFVRSNLKFQDAYNAAGHNA</th> <th>VFNFPNGTSHWEYV</th> <th>307</th>	ENFVRSNLKFQDAYNAAGHNA	VFNFPNGTSHWEYV	307
Db	251	WVYCGNGKPSDLGNNLPAKFL <th>EGFVRTSNIRKFDAYNAGG</th> <th>HGVDFDPDSTHSWEYV</th> <th>310</th>	EGFVRTSNIRKFDAYNAGG	HGVDFDPDSTHSWEYV	310
QY	308	GAQLNAMKGDLOSSLGA	324		
Db	311	GAQLNAMKPDLOALGA	327		
RESULT	28				
AAB82789	ID	AAB82789 standard; Protein; 338 AA.			
XX	AC	AAB82789;			
XX	DT	29-OCT-2001 (first entry)			
XX	DE	Mycobacterium tuberculosis antigen 85A.			
XX	KW	Mycobacterial antigen 85A; Ag85A; infection; vaccine; diagnosis; therapy.			
XX	KW	Mycobacterium tuberculosis.			
XX	OS	Mycobacterium tuberculosis.			
XX	FH	Key	Location/Qualifiers		
FT	FT	Peptide	48..56		
FT	FT	Peptide	/note= "epitope"		
FT	FT	Peptide	242..250		
XX	XX	Peptide	/note= "epitope"		
XX	PN	W0200158461-A1.			
XX	PD	16-AUG-2001.			
XX	PF	12-FEB-2001; 2001WO-GB00561.			
XX	PR	10-FEB-2000; 2000GB-0003082.			
XX	PA	(GLAX) GLAXO GROUP LTD.			
XX	PI	Dockrell HM, Smith SM, Brookes R;			
XX	DR	WPI; 2001-536505/59.			
XX	DR	N-PSDB; AAH26485.			
XX	PT	Use of polypeptides comprising groups of mycobacterial antigen 85A protein and expression vectors comprising polynucleotides encoding the polypeptide for vaccination against Mycobacterium tuberculosis.			
XX	PS	Disclosure; Page 42-43; 49pp; English.			
XX	CC	The present sequence is that of Mycobacterium tuberculosis antigen 85A (Ag85A). Epitopes of Ag85A, such as those including amino acids 48-56 or 252-250 of the present sequence (see AAB82787-88), have been identified which cause the generation of a strong CD8 T-cell response in humans. CD8 T-cells recognising such epitopes are able to lyse macrophages infected with live M. tuberculosis. A polypeptide which comprises an epitope structure of Ag85A, or an expression vector comprising a polynucleotide encoding such a polypeptide, is used in the manufacture of a medicament for vaccinating prophylactically or therapeutically against infection by a mycobacterium stimulating a CD8 T-cell response. The polypeptide or expression vector may be within an antigen-presenting cell. A claimed vaccine composition comprises the polypeptide or			

CC expression vector and an adjuvant or delivery system capable of
CC stimulating a CD8 T-cell response. Also claimed are methods of
CC detecting in a population of T-cells the presence or absence of CD8
CC T-cells that recognise the epitope sequence, a method of diagnosing
CC mycobacterial infection or of testing the effectiveness of a
CC vaccination, and a method of treating a mycobacterium infection by
CC administering T-cells capable of recognising the epitope.

XX SQ Sequence 338 AA;

Query Match 80.6%; Score 1407; DB 22; Length 338;
Best Local Similarity 78.9%; Pred. No. 3.5e-114;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 8 IRAGRELMTCTAAAVVLGLVGLAGGAATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 67
DB 11 VTGMSRLVVGAVGAALVGLVAVGTATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 70
QY 68 SGGNNSPAVLLDGLRAQDDYNGWDINTPAPEWYQSGLSIVMPVGGSSFYSDWYSPAC 127
DB 71 SGGANSFALYLLDGLRAQDDFSGWDINTPAPEWYDQSGLSVMPVGGSSFYSDWYQFAC 130
QY 128 GKACQYKWTFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILLAAVHPQOFIYAG 187
DB 131 GKACQYKWTFTLTSELPGWLQANRHVKPTGSAVGLSMAASSALTILAIYHPQOFVYAG 190
QY 188 SLSALLDPSQMGPSLIGLAMDAGGYKAAADWMPGSSDPWERNPTQOIIPKLIVANNTRL 247
DB 191 AMSGLDPSQMGPTLIGLAMDAGGYKASDMWGPKEDEPAWQRNDPLINVGKLIANNTRV 250
QY 248 WYCGNGTNPNEGNIIPAEFLENFVRSSNLKFQDAYNAAGHNAVENFPNGTHSWEYW 307
DB 251 WYCGNGKPSDLGGNNLPKAELEGFVRTSNIKFQDAYNAGGCHNGVDFPDGTHSWEYW 310
QY 308 GAQLNAMKGDLOSSLGA 324
DB 311 GAQLNAMKPDLOALGA 327

RESULT 29
ABB73458
ID ABB73458 standard; Protein; 338 AA.
XX AC ABB73458;
XX DT 08-APR-2002 (first entry)
XX DE M tuberculosis 85A protein SEQ ID NO: 32.

XX skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory.

XX Mycobacterium tuberculosis.

XX US6328978-B1.

XX 11-DEC-2001.

XX 02-JUN-1999; 99US-0324542.

XX 23-DEC-1997; 97US-0997080.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Tan PLJ, Prestidge R;

XX WPI; 2002-138361/18.

XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae

PT culture filtrate -

XX Example 5; Column 59-62; 116pp; English.

XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC protein described in the exemplification of the invention.

XX SQ Sequence 338 AA;

Query Match 80.6%; Score 1407; DB 23; Length 338;
Best Local Similarity 78.9%; Pred. No. 3.5e-114;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 8 IRAGRELMTCTAAAVVLGLVGLAGGAATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 67
DB 11 VTGMSRLVVGAVGAALVGLVAVGTATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 70
QY 68 SGGNNSPAVLLDGLRAQDDYNGWDINTPAPEWYQSGLSIVMPVGGSSFYSDWYSPAC 127
DB 71 SGGANSFALYLLDGLRAQDDFSGWDINTPAPEWYDQSGLSVMPVGGSSFYSDWYQFAC 130
QY 128 GKACQYKWTFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILLAAVHPQOFIYAG 187
DB 131 GKACQYKWTFTLTSELPGWLQANRHVKPTGSAVGLSMAASSALTILAIYHPQOFVYAG 190
QY 188 SLSALLDPSQMGPSLIGLAMDAGGYKAAADWMPGSSDPWERNPTQOIIPKLIVANNTRL 247
DB 191 AMSGLDPSQMGPTLIGLAMDAGGYKASDMWGPKEDEPAWQRNDPLINVGKLIANNTRV 250
QY 248 WYCGNGTNPNEGNIIPAEFLENFVRSSNLKFQDAYNAAGHNAVENFPNGTHSWEYW 307
DB 251 WYCGNGKPSDLGGNNLPKAELEGFVRTSNIKFQDAYNAGGCHNGVDFPDGTHSWEYW 310
QY 308 GAQLNAMKGDLOSSLGA 324
DB 311 GAQLNAMKPDLOALGA 327

RESULT 30
ABB73460
ID ABB73460 standard; Protein; 338 AA.
XX AC ABB73460;
XX DT 08-APR-2002 (first entry)
XX DE M bovis 85A protein SEQ ID NO: 34.

XX skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory.

XX Mycobacterium bovis.

XX US6328978-B1.

XX 11-DEC-2001.

XX 02-JUN-1999; 99US-0324542.

XX 23-DEC-1997; 97US-0997080.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Tan PLJ, Prestidge R;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:35:17 ; Search time 21.6667 Seconds
(without alignments)
1442.530 Million cell updates/sec

Title: US-09-805-427A-2
Perfect score: 1745
Sequence: 1 MTDVSRKIRAWGRRLMIGTA.....YWGALNAMKGLQSSLCAG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283102

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database :

PIR_76.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1745	100.0	325	2 C70516	probable fbpB prot
2	1739	99.7	325	2 S29663	antigen 85-B precu
3	1706	97.8	323	2 A32348	alpha-antigen B pr
4	1609	92.2	325	2 A37185	alpha-antigen prec
5	1539	88.2	330	2 JN0897	alpha-antigen prec
6	1519	87.0	330	2 S32773	alpha-antigen - My
7	1455	83.4	327	2 G87162	antigen 85A, mycol
8	1454	83.3	327	2 S34434	antigen 85-B - Myc
9	1428	81.8	327	2 S20038	fibronectin-bindin
10	1407	80.6	338	2 S10326	alpha-antigen A, e
11	1407	80.6	338	2 H70887	32K antigen fbpA p
12	1338.5	76.7	330	2 A86921	antigen 85A, mycol
13	1198	68.7	340	2 D70615	antigen fbpC2 - My
14	1170	67.0	333	2 S32114	85C protein - Myco
15	775	44.4	188	2 S32107	fbpC1 protein prec
16	519	29.7	299	2 G70887	antigen 85C, mycol
17	498.5	28.6	301	2 B86921	cspl protein - Cor
18	474	27.2	657	2 S25184	MPT51 protein - My
19	367.5	21.1	220	2 S32111	antigen 85-C - Myc
20	257	14.7	57	2 B43603	hypothetical prote
21	233.5	13.4	342	2 T29115	hypothetical prote
22	146.5	8.4	456	2 D70772	tributyrin esteras
23	143	8.2	259	2 E95071	tributyrin esteras
24	143	8.2	259	2 C97939	acetyltransferase hom
25	134	7.7	252	2 AB1748	lipase [imported]
26	133	7.6	252	2 A11378	hypothetical prote
27	132	7.6	258	2 C86846	alpha-antigen C, e
28	129.5	7.4	76	2 A70716	
29	128	7.3	26	2 C41499	

ALIGNMENTS

RESULT 1

C70516

probable fbpB protein - Mycobacterium tuberculosis (strain H37RV)

N:Alternate names: antigen 85-B precursor

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C:Accession: C70516; S29664

probable membrane
antigen A 31K comp
S-formylglutathion
probable esterase
esterase/lipase (i
tributyrin esteras
prolyl oligopeptid
probable esterase
transferred entry
esterase sll0992 -
poly(3-hydroxybuty
hypothetical prote
probable transmem
hypothetical prote
carboxylesterase (i
methylesterase (i
hypothetical prote
probable esterase
carboxylesterase (i
transforming prote
hypothetical prote
hypothetical prote
regulatory protein
esterase [imported
hypothetical prote
hypothetical prote
YalM protein - Esc
proteoglycan core
aggreca - bovine
cellulase (EC 3.2.
probable transmem
hypothetical prote
probable pyrophosp
hypothetical prote
porin P precursor,
outer membrane por
poly(3-hydroxybuty
probable esterase
probable lpqr prot
conserved hypothet
lep1170 F3.112 pr
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypothet
conserved hypothet
period clock prote
branched-chain ami
diene lactone hydro
hypothetical prote
pectate lyase (EC
pyruvate, phosphat
conserved hypothet
cellulose 1,4-beta
hypothetical prote
probable photosyst
and cellulose-bind

30	125	7.2	377	2	T36322
31	116	6.6	26	2	A44892
32	113	6.5	282	2	A12156
33	112	6.4	284	2	T00809
34	111	6.4	322	2	A28222
35	111	6.4	322	2	E97600
36	111	6.4	618	2	D87651
37	109	6.2	363	2	T36408
38	109	6.2	827	2	JC4900
39	108	6.2	276	2	S75249
40	107.5	6.2	689	2	A21222
41	106	6.1	414	2	S39530
42	105.5	6.0	293	2	C90032
43	105.5	6.0	415	2	T36279
44	105	6.0	430	2	B81633
45	104	6.0	280	2	A10192
46	104	6.0	297	2	A23543
47	104	6.0	963	2	T40290
48	103.5	5.9	277	2	B0680
49	103.5	5.9	277	2	F85530
50	102	5.8	1106	1	TVHUGL
51	100.5	5.8	328	2	C87451
52	100.5	5.8	426	2	S28812
53	99.5	5.7	555	1	RGASWA
54	98.5	5.6	277	2	B87561
55	98	5.6	472	2	C75505
56	98	5.6	1501	2	T45623
57	97.5	5.6	277	2	C64763
58	97.5	5.6	1340	2	A39808
59	97.5	5.6	2327	2	T42630
60	97	5.6	264	2	JU0328
61	97	5.6	344	2	T36160
62	97	5.6	359	2	H70876
63	97	5.6	794	2	T36668
64	96.5	5.5	631	2	B83404
65	95.5	5.5	440	2	S11793
66	95.5	5.5	440	2	F83235
67	95.5	5.5	488	2	A32235
68	95	5.4	285	2	AB0782
69	95	5.4	452	2	F70552
70	94.5	5.4	358	2	B87063
71	94.5	5.4	391	2	S72717
72	94	5.4	312	2	A70708
73	94	5.4	489	2	B70619
74	94	5.4	567	2	AF0308
75	94	5.4	593	2	T01575
76	93.5	5.4	352	2	S72984
77	93.5	5.4	420	2	AG1859
78	93.5	5.4	473	2	E86955
79	93.5	5.4	884	2	E75489
80	93.5	5.4	1122	2	B26427
81	93	5.3	424	2	G75579
82	92.5	5.3	323	2	G87358
83	92.5	5.3	536	2	A99283
84	92.5	5.3	677	2	JC7303
85	92	5.3	601	2	E87028
86	92	5.3	786	2	E87565
87	92	5.3	1230	2	S47466
88	91.5	5.2	299	2	S50803
89	91.5	5.2	403	2	T51828
90	91.5	5.2	537	2	B97013

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, K.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.R.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70516
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-325 <COL>
A:Cross-references: GB:297193; GB:AL123456; NID:g3261816; PIDN:CAB10044.1; PID:g2225974
A:Experimental source: Strain H37Rv
R:de Wit, L.; Palou, M.; Content, J.
submitted to the EMBL Data Library, December 1991
A:Reference number: S29663
A:Accession: S29664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <WIT>
A:Cross-references: EMBL:X62398; NID:g44563; PIDN:CAA44269.1; PID:g44564
C:Genetics:
A:Gene: fbpB
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 100.0%; Score 1745; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.4e-126; Mismatches 0; Indels 0; Gaps 0;
Matches 325; Conservative 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180
Db 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180
QY 181 QOFIYAGLSALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPFAWERNDPTQOIPLK 240
Db 181 QOFIYAGLSALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPFAWERNDPTQOIPLK 240
QY 241 VANNTLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANNTLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
QY 301 THSWEYWGALNAMKGDLOSSLGAG 325
Db 301 THSWEYWGALNAMKGDLOSSLGAG 325

RESULT 2

S29663
antigen 85-B precursor - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000
R:de Wit, L.; Palou, M.; Content, J.
submitted to the EMBL Data Library, December 1991
A:Reference number: S29663
A:Accession: S29663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <WIT>
A:Cross-references: EMBL:X62397; NID:g44167; PIDN:CAA44268.1; PID:g44168
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 99.7%; Score 1739; DB 2; Length 325;
Best Local Similarity 99.7%; Pred. No. 7e-126;
Matches 324; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180
Db 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180
QY 181 QOFIYAGLSALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPFAWERNDPTQOIPLK 240
Db 181 QOFIYAGLSALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPFAWERNDPTQOIPLK 240
QY 241 VANNTLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANNTLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
QY 301 THSWEYWGALNAMKGDLOSSLGAG 325
Db 301 THSWEYWGALNAMKGDLOSSLGAG 325

RESULT 3

A32348
alpha-antigen B precursor, extracellular - Mycobacterium bovis
N:Alternate names: 32k antigen
C:Species: Mycobacterium bovis
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 26-May-2000
A:Accession: A32348; A41499; A60278
R:Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Yamada, T.
J. Bacteriol. 170, 3847-3854, 1988
A:Title: Cloning and expression of the Mycobacterium bovis BCG gene for extracellular
A:Reference number: A32348; MUID:86314872; PMID:2842287
A:Accession: A32348
A:Molecule type: DNA
A:Residues: 1-323 <MA>
A:Cross-references: GB:M21839; NID:g149935; PIDN:AAA25359.1; PID:g149936
R:Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A:Title: Evidence for three separate genes encoding the proteins of the mycobacterial
A:Reference number: A41499; MUID:90093478; PMID:2403534
A:Accession: A41499
A:Molecule type: protein
R:Rifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A:Title: Purification and characterization of major antigens from a Mycobacterium bovis
A:Reference number: A60278; MUID:91147217; PMID:1900061
A:Accession: A60278
A:Molecule type: protein
A:Residues: 41-59 <PIF>
C:Superfamily: Mycobacterium avium alpha-antigen
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-323/Product: alpha antigen, extracellular #status experimental <MAT>

Query Match 97.8%; Score 1706; DB 2; Length 323;
Best Local Similarity 98.5%; Pred. No. 2.3e-123;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180

Db 121 DWSPACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
 Db 181 QOPIYAGLSALLDPSQGMG--LIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 238
 QY 241 VANNTLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
 Db 239 VANNTLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNPAGGHNAVFPPNG 298
 QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
 Db 299 THSWEYGAQLNAMKGDLOSSLGAG 323

RESULT 4

A37185

alpha-antigen precursor - Mycobacterium kansasii
 C:Species: Mycobacterium kansasii

C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 26-May-2000

C:Accession: A37185

R;Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Terasaka, K.; Yamada, T.

Infect. Immun. 58, 550-556, 1990

A;Title: Cloning and expression of the gene for the cross-reactive alpha antigen of Myc

A;Reference number: A37185; MUID:90129315; PMID:2404875

A;Accession: A37185

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 <MAT>

A;Cross-references: GB:M53897

C;Superfamily: Mycobacterium avium alpha-antigen

Query Match 92.2%; Score 1609; DB 2; Length 325;
 Best Local Similarity 89.8%; Pred. No. 6.4e-116;
 Matches 291; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
 Db 1 MTDVSGKIRAWGRRLLVGAATAAALPGLVGLAGGAATAGAFSRPGLPVEYLQVPSAAMGR 60
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 Db 61 SIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 QY 121 DWSPACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 Db 121 DWSPACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
 Db 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
 QY 241 VANNTLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
 Db 241 VANNTLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
 QY 301 THSWEYGAQLNAMKGDLOSSLGAG 324
 Db 301 THSWEYGAQLNAMKGDLOSSLGAG 324

RESULT 5

JN0897

alpha-antigen precursor - Mycobacterium intracellulare
 N;Alternate names: A985B

C:Species: Mycobacterium intracellulare

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 26-May-2000

C:Accession: JN0897

R;Kitaura, H.; Ohara, N.; Matsuo, T.; Tasaka, H.; Kobayashi, K.; Yamada, T.

Biochem. Biophys. Res. Commun. 196, 1466-1473, 1993

A;Title: Cloning, sequencing and expression of the gene for alpha antigen from Mycobacte

A;Reference number: JN0897; MUID:94071912; PMID:8250904

A;Accession: JN0897

A;Molecule type: DNA

A;Residues: 1-330 <KIT>

C;Comment: This protein is one of antigen 85.

C;Comment: This protein is an important stimulant of cellular and humoral immunity and

C;Superfamily: Mycobacterium avium alpha-antigen

F;1-40/Domain: signal sequence #status predicted <SIG>

F;41-330/Product: alpha-antigen #status predicted <PAA>

Query Match 88.2%; Score 1539; DB 2; Length 330;
 Best Local Similarity 85.8%; Pred. No. 1.5e-110;
 Matches 278; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
 Db 1 MTDLSEKVRWGRRLVVGAAAATLPLGLIAGGAATANAFSRPGLPVEYLQVPSAGMGR 60
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 QY 121 DWSPACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 Db 121 DWYQACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
 Db 181 NQFVYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPAL 240
 QY 241 VANNTLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
 Db 241 VGNTRLWYVCGNGTNPGLGANNIPAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
 QY 301 THSWEYGAQLNAMKGDLOSSLGAG 324
 Db 301 THSWEYGAQLNAMKGDLOSSLGAG 324

RESULT 6

S32773

alpha-antigen - Mycobacterium avium

C:Species: Mycobacterium avium

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000

C;Accession: S32773

R;Ohara, N.; Matsuo, K.; Yamaguchi, R.; Yamazaki, A.; Tasaka, H.; Yamada, T.

submitted to the EMBL Data Library, December 1991

A;Description: Nucleotide sequence of the alpha-antigen gene of Mycobacterium avium.

A;Reference number: S32773

A;Accession: S32773

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-330 <OHA>

A;Cross-references: EMBL:X63437

C;Superfamily: Mycobacterium avium alpha-antigen

Query Match 87.0%; Score 1519; DB 2; Length 330;
 Best Local Similarity 84.6%; Pred. No. 5.1e-109;
 Matches 274; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
 Db 1 MTDLSEKVRWGRRLVVGAAAATLPLGLIAGGAATANAFSRPGLPVEYLQVPSAGMGR 60
 QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
 QY 121 DWSPACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 Db 121 DWYQACGKAGCQTYKWTETLTSELPAWLSANRAVKTGSAALGLSMAGSSAMILAAVHP 180
 QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
 Db 181 DQFIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240

QY	241	VANNRLWVYCGNGTPEINELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPENG	300
Db	241	VGNTRLWLTCNGTTPSEVGGANPAEFLENFVRSSNLKFQDAYNAGGHNNAVFNPENG	300
QY	301	THSWEYGAQINAMKGLQSSLGA	324
Db	301	THSWEYGAQINAMKPDLOGTGA	324

RESULT 7
antigen 85A, mycolyltransferase [imported] - Mycobacterium leprae G87162
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: G87162
R: Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HC
R.: Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
ature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; SQ
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: G87162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <STO>
A:Cross-references: GB:AL450380; NID:g13093650; PIDN:CAC30983.1; GSPDB:GN00147
C:Genetics:
A:Gene: fbpB
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match	83.4%;	Score 1455;	DB 2;	Length 327;
Best Local Similarity	83.0%;	Pred. No. 4e-104;		
Matches 269;	Conservative 19;	Mismatches 34;	Indels 2;	Gaps 1;

QY	1	MTDVS	KTR	AWGR	RLMI	GTA	AAV	U	PG	L	VL	G	AG	GA	T	A	G	A	F	S	R	P	G	L	P	VE	Y	L	Q	V	S	E	S	M	G	R	60																				
DB	1	MIDV	G	K	T	R	A	W	G	R	L	L	W	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	U	58																						
QY	61	DI	K	V	F	Q	S	G	G	N	N	S	P	A	V	I	L	D	L	G	R	A	D	D	Y	N	G	M	D	I	N	T	P	A	F	E	Y	Y	Q	S	L	I	V	M	P	V	G	G	O	S	S	F	Y	S	120		
DB	59	SI	K	V	F	Q	S	G	G	N	N	S	P	A	V	I	L	D	L	G	R	A	D	D	Y	N	G	M	D	I	N	T	P	A	F	E	Y	Y	Q	S	L	I	V	M	P	V	G	G	O	S	S	F	Y	S	118		
QY	121	DW	S	P	A	C	K	A	G	C	T	Y	K	W	E	T	F	L	S	E	L	P	O	M	L	S	A	N	R	A	V	K	P	T	G	S	A	I	G	H	S	M	A	G	S	S	A	M	I	L	A	A	Y	H	P	180	
DB	119	DW	S	P	A	C	K	A	G	C	T	Y	K	W	E	T	F	L	S	E	L	P	O	M	L	S	A	N	R	S	V	K	T	G	S	A	V	V	G	L	S	M	A	G	S	S	A	M	I	L	A	A	Y	H	P	178	
QY	181	Q	F	I	A	G	S	L	S	A	L	I	D	P	S	C	M	G	P	S	L	I	G	L	A	M	D	A	G	G	Y	K	A	A	D	M	W	G	P	S	S	P	A	W	E	R	N	D	P	T	O	O	I	P	K	L	240
DB	179	D	Q	F	I	A	G	S	L	S	A	L	I	D	P	S	C	M	G	P	S	L	I	G	L	A	M	D	A	G	G	Y	K	A	A	D	M	W	G	P	S	S	P	A	W	E	R	N	D	P	I	L	Q	A	G	L	238
QY	241	V	A	N	N	T	L	W	Y	C	G	N	T	P	E	I	L	G	G	N	I	P	A	E	F	L	E	N	V	R	S	N	L	K	F	O	D	A	Y	N	A	A	G	H	N	A	V	E	N	F	P	P	N	G	300		
DB	239	V	A	N	N	T	L	W	Y	C	G	N	T	P	E	I	L	G	G	N	I	P	A	E	F	L	E	N	V	F	H	G	S	N	L	K	F	O	D	A	Y	N	A	A	G	H	N	A	V	E	N	F	N	A	D	G	298
QY	301	T	H	S	W	E	Y	G	A	Q	L	N	A	M	K	D	G	L	O	S	S	L	G	A	324																																
DB	299	T	H	S	W	E	Y	G	A	Q	L	N	A	M	K	P	D	L	O	N	T	L	M	A	322																																

RESULT 8
S34434
antigen 85-B - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-May-2000
R:Accession: S34434
R:de Mendonca Lima, L.; Content, J.; van Heuverswyn, H.; Degraeve, W.
Nucleic Acids Res. 19, 5789, 1991
A:Title: Nucleotide sequence of the gene coding for the 85-B antigen of Mycobacterium leprae
A:Reference number: S34434; MUID:92051335; PMID:1945858
A:Accession: S34434
A>Status: preliminary

A;Molecule type: DNA
A;Residues: 1-327 <DEM>
A;Cross-references: EMBL:X60934; NID:g44380; PDB:CAA43269.L; PDB:g44381
C;Superfamily: Mycobacterium avium alpha-antigen

Query Match	83.3%;	Score 1454;	DB 2;	Length 327;
Best Local Similarity	83.0%;	Pred. No. 4.8e-104;		
Matches 269;	Conservative	19;	Mismatches 34;	Indels 2;
				Gaps 1;

Qy	1	MTDVS	KIRAWGRRL	MLGITRAAAV	LPGLV	CLAGGAATAGAFSPG	LPVEVYLQVPS	PMGR	60
Db	1	MIDVSG	KIRAWGRWLLV	G--AAAT	LP	SLISLAGGAATASAFSPG	LPVEVYLQVPS	EMGR	58
Qy	61	DIKVF	QFSGGNN	SPAVLLD	DGLRA	DDYNGWDINTPAF	WYIOGSLIVMP	VGGQSSFY	120
Db	59	TIKVF	QFONGG	SPAVLLD	DGLRA	DDYNGWDINTSAF	WYIOGSLIVMP	VGGQSSFY	118
Qy	121	DWTS	PACGKAGC	OTYKWE	TLSL	POWLSANRAVKPTG	SAATIGLSMAGS	SAMILAA	180
Db	119	DWTS	PACGKAGC	TTIKWE	TLSL	PKWLSANRSVKSTG	SAVVGLSMAGS	SALLIAA	178
Qy	181	QQFI	YAGSL	SALLDPS	QGMG	PSLIGLAWG	DAGGYKAADMMG	PSDDPAWERN	240
Db	179	DQFI	YAGSL	SALMDSS	QIEP	FLQILGLAWG	DAGGYKAADMMG	PNDPAWQRND	238
Qy	241	VANN	TRLVVY	CNGT	PNEL	GANTPAE	FLNFVSSNLKF	ODAYNAAGG	300
Db	239	VANN	THLVVY	CNGT	PNSEL	GGTVNPAE	FLNFVHGSNLKF	ODAYNGAGG	298
Qy	301	THSWEY	GGAQLNAM	KD	LQSS	LG			324
Db	299	THSWEY	GGAQLNAM	KP	LQNT	IMA			322

RESULT 9

S20038
fibronectin-binding antigen 85 precursor - Mycobacterium leprae
C.Species: Mycobacterium leprae
C.Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 26-May-2000
C.Accession: S20038; S77953
R.Thole, J.E.R.; Schoeningh, R.; Janson, A.A.M.; Garbe, T.; Cornelisse, Y.E.; Clark-Cu-
Mol. Microbiol. 6, 153-163, 1992
A.Title: Molecular and immunological analysis of a fibronectin-binding protein antigen
A.Reference number: S20038; MUID:92186705; PMID:1532043
A.Accession: S20038
A.Molecule type: DNA
A.Residues: 1-327 <THO>
A.Cross-references: EMBL:Z11666
R.Thole, J.E.R.
submitted to the EMBL Data Library, January 1992
A.Reference number: S77953
A.Accession: S77953
A.Molecule type: DNA
A.Residues: 1-63, 'F', 65-327 <THW>
A.Cross-references: EMBL:Z11666
C.Superfamily: Mycobacterium avium alpha-antigen
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-327/Product: fibronectin-binding antigen 85 #status predicted <MAT>
F;55-266/Region: fibronectin-binding
F;265-327/Region: fibronectin-binding

Query Match	81.8%;	Score 1428;	DB 2;	Length 327;
Best Local Similarity	81.8%;	Pred. No. 4.7e-102;		
Matches 265:	Conservative	20;	Mismatches 37;	Indels 2;
	Gaps	1;		

[illegible]

QY 121 DWSPACGKAGCCTYKWTETLTSELPWLSANRAVKPTGSAALIGLSMAGSAMILAAAYHP 180
Db 119 DWSPACGKAGCCTYKWTETLTSELPKCVSANRSVKSTGRVVLGSLWAGSALILAAAYHP 178
QY 181 QOFTYAGSLGALDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPSDPAWERNNDPTQOIQPKL 240
Db 179 DQFTYAGSLGALDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPNDPAWQRNDPILQAGKL 238
QY 241 VANNRLWVYCGNGTPELGGANIPAEFLNFVRSSNLKFDQDAYNAAGGHNAPVFPNG 300
Db 239 VANNRLWVYCGNGTPELGGTNNVPAEFLNFVRSSNLKFDQDAYNAAGGHNAPVFPNG 298
QY 301 THSWEYWGALQNAKMGDLQSSSLGA 324
Db 299 THSWEYWGALQNAKMPDLQNTLMA 322

RESULT 10
S10326
alpha-antigen A, extracellular - Mycobacterium bovis
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 26-May-2000
C:Accession: S10326; B41499
R:De Wit, L.; de la Cuvelier, A.; Ooms, J.; Content, J.
Nucleic Acids Res. 18, 3995, 1990
A:Title: Nucleotide sequence of the 32 kDa-protein gene (antigen 85 A) of Mycobacterium
A:Reference number: S10326; MUID:90326531; PMID:2197602
A:Accession: S10326
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <WIT>
A:Cross-references: EMBL:X53034; NID:g44165; PIDN:CAA37206.1; PID:g44166
R:Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A:Title: Evidence for three separate genes encoding the proteins of the mycobacterial an
A:Reference number: A41499; MUID:90093478; PMID:2403534
A:Accession: B41499
A>Status: preliminary
A:Molecule type: protein
A:Residues: 44-82 <WIK>
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 80.6%; Score 1407; DB 2; Length 338;
Best Local Similarity 78.9%; Pred. No. 2e-100;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 8 IRWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGRDIAKVFQ 67
Db 11 VTGMSRRLVVGAVGAALVSLGAVGGTATAGAFSRPGLPVEYLQVPSMGRDIAKVFQ 70
QY 68 SGNNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGQSSFYSDWYSPAC 127
Db 71 SGANSPLYLLDGLRAQDDFGSDINTPAFEWYQSGLSIVMPVGGQSSFYSDWYSPAC 130
QY 128 GKAGCTYKWTETLTSELPWLSANRAVKPTGSAALIGLSMAGSAMILAAAYHPQFIYAG 187
Db 131 GKAGCTYKWTETLTSELPWLSANRAVKPTGSAALIGLSMAGSAMILAAAYHPQFIYAG 190
QY 188 SLGALLDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPSDPAWERNNDPTQOIQPKLVANNRL 247
Db 191 AMSGLLDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPSDPAWERNNDPTQOIQPKLVANNRL 250
QY 248 WYCGNGTPELGGANIPAEFLNFVRSSNLKFDQDAYNAAGGHNAPVFPNGTHSWEY 307
Db 251 WYCGNGKPSDLGGNNLPKAFLEGFVRTSNIKFDQDAYNAAGGHNAPVFPNGTHSWEY 310
QY 308 GAQLNAKMGDLQSSSLGA 324
Db 311 GAQLNAKMPDLQRAUGA 327

RESULT 11
H70887

32K antigen fbpA precursor - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 30K native antigen; major protein antigen MPT45
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: H70887; A37024; G60274; A54318
R:Coale, S.T.; Brosch, R.; Farkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, R.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:9825987; PMID:9634230
A:Accession: H70887
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-338 <COL>
A:Cross-references: GB:AL022076; GB:AL123456; NID:g3256026; PIDN:CAA17868.1; PID:g295042
R:Experimental source: strain H37RV
R:Borreman, M.; De Wit, L.; Volckaert, G.; Ooms, J.; De Bruyn, J.; Huygen, K.; Van Voor
Infect. Immun. 57, 3123-3130, 1989
A:Title: Cloning, sequence determination, and expression of a 32-kilodalton-protein gene
A:Reference number: A37024; MUID:89379378; PMID:2506131
A:Accession: A37024
A:Molecule type: DNA
A:Residues: 1-23,25; R', 27-130; R', 132-291; R', 293-323; HWVPRPTP, 332-333, 335-338 <BOR>
A:Cross-references: GB:M27016; GB:X53898
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; MUID:91099989; PMID:1898899
A:Accession: C60274
A:Molecule type: protein
A:Residues: 44-48 <NAG>
R:Salata, R.A.; Sanson, A.J.; Malhotra, I.J.; Wiker, H.G.; Harboe, M.; Phillips, N.B.; D.
J. Lab. Clin. Med. 118, 589-598, 1991
A:Title: Purification and characterization of the 30,000 dalton native antigen of Mycobac
tigen.
A:Reference number: A54318; MUID:92078747; PMID:1720803
A:Accession: A54318
A>Status: preliminary
A:Molecule type: protein
A:Residues: 44-63 <SAL>
A:Experimental source: H37Ra
A:Note: sequence extracted from NCBI backbone (NCBIP:68909)
C:Genetics:
A:Gene: fbpA
C:Superfamily: Mycobacterium avium alpha-antigen
F:1-43/Domain: signal sequence #status predicted <SIG>
F:44-338/Product: 32K antigen fbpA #status experimental <MAT>

Query Match 80.6%; Score 1407; DB 2; Length 338;
Best Local Similarity 78.9%; Pred. No. 2e-100;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 8 IRWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGRDIAKVFQ 67
Db 11 VTGMSRRLVVGAVGAALVSLGAVGGTATAGAFSRPGLPVEYLQVPSMGRDIAKVFQ 70
QY 68 SGNNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGQSSFYSDWYSPAC 127
Db 71 SGANSPLYLLDGLRAQDDFGSDINTPAFEWYQSGLSIVMPVGGQSSFYSDWYSPAC 130
QY 128 GKAGCTYKWTETLTSELPWLSANRAVKPTGSAALIGLSMAGSAMILAAAYHPQFIYAG 187
Db 131 GKAGCTYKWTETLTSELPWLSANRAVKPTGSAALIGLSMAGSAMILAAAYHPQFIYAG 190
QY 188 SLGALLDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPSDPAWERNNDPTQOIQPKLVANNRL 247
Db 191 AMSGLLDPSQGMGSPSLIGLWAGDAGGYKAADMMGPPSDPAWERNNDPTQOIQPKLVANNRL 250
QY 248 WYCGNGTPELGGANIPAEFLNFVRSSNLKFDQDAYNAAGGHNAPVFPNGTHSWEY 307
Db 251 WYCGNGKPSDLGGNNLPKAFLEGFVRTSNIKFDQDAYNAAGGHNAPVFPNGTHSWEY 310

[illegible]

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Db 79 -AVYLLDGLRAQEDYNGWDINIPAEFYHSLGSLVMPGGQSSFSYWNYPQSQNGQHY 137
QY 134 TYKWTFTLTSELPOWLSANRAVKTGSAAGLSMAGSSAMILAAHYHPQOFTYAGLSALL 193
Db 138 TYKWTFTLTQEMPSLQANKNVLPTGNAAGVLSMGSALILASVYPQOFPYAASLSGFL 197
QY 194 DPSQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKLIVANNTRLMVYCGN 253
Db 198 NPSEGWTMTGLANDSGGVNANSMWGPSTDPANERNDPTQOIPKLIVANNTRLMVYCGN 257
QY 254 GTPNELGANIPAEFLNFVRSNLFQDAYNAAGGHNAVFNPNGTHSWEYWGQAQLNA 313
Db 258 GAPNELGDNIPAKFLESILTSTNIFQNTYAASGRGVNFNPNGTHSWEYWGQAQLNA 317
QY 314 MKGDLQSSL 322
Db 318 MKPDIQQL 326

RESULT 15
S32107
85A protein - Mycobacterium leprae (fragment)
C:Species: Mycobacterium leprae
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jun-2000
C:Accession: S32107
R:Rinke de Wit, T.F.; Bekelie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, J.E.R.
submitted to the EMBL Data Library, March 1993
A:Description: The M.leprae antigen 85 complex gene family: identification of the genes
A:Reference number: S32107
A:Accession: S32107
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <RIN>
A:Cross-references: EMBL:Z21950; NID:g287919; PIDN:CAA79948.1; PID:g287920
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 44.4%; Score 775; DB 2; Length 188;
Best Local Similarity 75.0%; Pred. No. 2.7e-52;
Matches 138; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 141 LTSELPOWLSANRAVKTGSAAGLSMAGSSAMILAAHYHPQOFTYAGLSALLDPSQGMG 200
Db 1 LTSELPOYLSQNKQIKPTGSAAGVLSMAGLSALTALYHPDQFTYVGSMSGLDPSNMG 60
QY 201 PSLIGLAMGDAGGYKAADMWGPSSDPANERNDPTQOIPKLIVANNTRLMVYCGNTPNELG 260
Db 61 PSLIGLAMGDAGGYKAADMWGPSSDPANERNDPTQOIPKLIVANNTRLMVYCGNTPNELG 120
QY 261 GANIPAEFLNFVRSNLFQDAYNAAGGHNAVFNPNGTHSWEYWGQAQLNAMKGDLS 320
Db 121 GNNLPKLLLEGLVRSNLFQDAYNAAGGHNAVFNPNGTHSWEYWGQAQLNAMKGDLS 180
QY 321 SLGA 324
Db 181 YLGA 184

RESULT 16
G70887
fbpC1 protein precursor - Mycobacterium tuberculosis
N:Alternate names: major antigen MPTs1
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: G70887; A60274
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70887

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A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <COL>
A:Cross-references: GB:AL022076; GB:AL123456; NID:g3256026; PIDN:CAA17867.1; PID:g29504
A:Experimental source: strain H3/RV
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture
A:Reference number: A60274; MUID:9109989; PMID:1898899
A:Accession: A60274
A>Status: preliminary
A:Molecule type: protein
A:Residues: 34-40,'Y',42-49,'K',51-58;59-76;77-78 <NAG>
C:Genetics:
A:Gene: fbpC1
C:Superfamily: Mycobacterium avium alpha-antigen
F:34-299/Product: fbpC1 protein #status experimental <MAT>

Query Match 29.7%; Score 519; DB 2; Length 299;
Best Local Similarity 38.7%; Pred. No. 1.9e-32;
Matches 113; Conservative 39; Mismatches 124; Indels 16; Gaps 5;

QY 33 GGAATAGAFSRPGLPVEYLQVPSMGRDVKVQFQSGNNSPAVYLLDGLRAQDDYNGWD 92
Db 21 GGVAFAAEPTAKAAPYENLWVPSMGRDIPVAFLAGGPH--AVYLLDAFNAGPDVSNVW 78
QY 93 INTFAEWYQSGLSIVMPYVGGSSFFSDWVSPACGKAGCOTYKWFELTSELPOWLSAN 152
Db 79 TAGNANTLAKGLSVVAPAGGAYMTNWEQD-----SKOWDTFLSAELPDWLAAN 131
QY 153 RAVKPTGSAAGLSMAGSSAMILAAHYHPQOFTYAGLSALLDPSQGMPSLIGLAMGDAG 212
Db 132 RGLAPGHAAGVAAQGGYGMAALAAHPDRFGFAGSSMGFLYPSNTTNGAIAAGMOQFG 191
QY 213 GYKAAADWGPSSDPANERNDPTQOIPKLIVANNTRLMVYCGNTPNELGANIPAEFLNF 272
Db 192 GVDITNGWGAPOQLGRWKWHDPMVHASLLAQNNTRVWVW---SPTN-PGASDPAAMTGOA 246
QY 273 VRS--SNLKFQDAYNAAGGHNAVFNPNGTHSWEYWGQAQLNAMKGDLSL 322
Db 247 AEANGSRMPYQYRSVGGHNGHFDPPASGDNMGWGWAPQLGAMSGDIVGAI 298

RESULT 17
B86921
antigen 85C, mycolyltransferase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B86921
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-
eam, M.A.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: B86921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <STO>
A:Cross-references: GB:AL450380; NID:gi3092480; PIDN:CAC29606.1; GSPDB:GNO0147
C:Genetics:
A:Gene: fbpC
C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 28.6%; Score 498.5; DB 2; Length 301;
Best Local Similarity 38.7%; Pred. No. 7e-31;
Matches 120; Conservative 39; Mismatches 124; Indels 27; Gaps 8;

QY 15 LMIGTAAAVLPLGVLAGGAATAGAFSRPGLPVEYLQVPSMGRDVKVQFQSGNNSP 74
Db 16 LAAGVFAAAVL--LAGTAGNAKAAG-----YESLWVPSNAMGRDIPVAFWAGGPH-- 63

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75 AVYLLDGLRAODDYNWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPACGKAGCQT 134
 64 AVYLLDFAAFNAAVDVSNVVTAGNMTTLGGRGISVVPAGGAYSMYTNWENDG-----S 116
 135 YKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPQOFIYAGLSALLD 194
 117 KQWDTFUSSELPDWLTATKRGAPDGHAAVAGASQGGYALAAAHFDFRGFAGSLSGFVY 176
 195 PSQGMGPSLIGLAMGDAGGYKAAADMWGPSSDPAMERNPTQOIIPKLVANTRLVYCGNG 254
 177 PSTNYNGAILAGLQFGIDGNGMGAPQLGRWKHDPYVHAILAQNTRVWVY----- 232
 255 TPNELGGANIPAELENFVRS--SNLKFQDAYNAAGGNVAFNPPNGTHSWYWGQQLN 312
 233 SPMTMGG-DIDA-MIGQAVASGMSRBFYQYRSVGGHGHDFSGGSDNGWGAWAPQLA 290
 313 AMKGDQSSSL 322
 291 AMSGDIVGAI 300

RESULT 18
 S25184
 cspl protein - Corynebacterium glutamicum
 N:Alternate names: secreted protein PSI
 C:Species: Corynebacterium glutamicum
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Oct-1999
 C:Accession: S25184
 R:Joliff, G.; Mathieu, L.; Hahn, V.; Bayan, N.; Duchiron, F.; Renaud, M.; Shechter, E.;
 Mol. Microbiol. 6, 2349-2362, 1992
 A>Title: Cloning and nucleotide sequence of the cspl gene encoding PSI, one of the two
 cobacterium antigen 85 complex.
 A:Reference number: S25184; MUID:93023863; PMID:1406274
 A:Accession: S25184
 A:Molecule type: DNA
 A:Residues: 1-657 <JOL>
 A:Cross-references: EMBL:X66078; NID:G40486; PIDN:CAA46877.1; PID:G40487
 C:Genetics:
 A:Gene: cspl

Query Match 27.2%; Score 474; DB 2; Length 657;
 Best Local Similarity 36.1%; Pred. No. 1.3e-28;
 Matches 115; Conservative 40; Mismatches 140; Indels 24; Gaps 8;
 20 AAAYVPLGLVGLAGGAATAGAFRRPGLPVEYIQVPSPM-GRDIKVQ-----PQSGGN 71
 78 AGEVTYPEIAGLPDGVVRVISAEWATSKHV-ILTIQSAAMPERPIKVQLLLPRDWYSSPNR 136
 72 NSPANYLLDGLRAODDYNWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPACGKAG 131
 137 EFPEIWAIDGRIAEIOSQSWTIETNTIEQYADKNALIVLPIGESSFYSDWEEPNNGK-- 194
 132 CQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPQOFIYAGLSLSA 191
 195 --NYQWETLTQLAPILDKGFR-SNTDRAITGISMGGAIVNATHPDWMEKFGVSGFSG 251
 192 LLDPSQGMGPSLIGLAMGDAGGYKAAADMWGPSSDPAMERNPTQOIIPKLVANTRLVYVC 251
 252 YLDTTSAGMPIALSAALADAGGYDANAMWGPVGSERWQENDPKSNVDKL--KGTIIYVSS 309
 252 GNGTPN-----ELGANNIPAELENFVRSNLFQDAYNAAGGNVAFNPPNGTHSW 304
 310 GNGADDFGKEDSVAGFANATGVGLEVISMTSCQTFVDRANQA-GVEVVASFRPSPGVHSH 368
 305 EYWGAQINAMKGLQSSSLG 323
 369 EYQWFEMTQAPPHIANALG 387

RESULT 19
 S32111
 MPT51 protein - Mycobacterium leprae (fragment)
 C:Species: Mycobacterium leprae

C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Mar-2001
 C:Accession: S32111
 R:Rinke de Wit, T.F.; Bekellie, S.; Osland, A.; Wieles, B.; Janson, A.A.M.; Thole, J.B.R.
 submitted to the EMBL Data Library, March 1993
 A:Description: The M.leprae antigen 85 complex gene family: identification of the genes
 A:Reference number: S32107
 A:Accession: S32111
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <RIN>
 A:Cross-references: EMBL:Z21949; NID:G287923; PIDN:CAA79947.1; PID:9581345
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 21.1%; Score 367.5; DB 2; Length 220;
 Best Local Similarity 39.7%; Pred. No. 5.3e-21;
 Matches 87; Conservative 26; Mismatches 87; Indels 19; Gaps 4;
 15 LMIGTAAAVLPGLVGLAGGAATAGAFRRPGLPVEYIQVPSPMGRDIKVQFQSGNNNSP 74
 16 LAVGVFAAVL--LAGTAGNAKAG-----YESLMVPSNAMGRDIPVAFMAGGPH-- 63
 75 AVYLLDGLRAODDYNWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPACGKAGCQT 134
 64 AVYLLDFAAFNAAVDVSNVVTAGNMTTLGGRGISVVPAGGAYSMYTNWENDG-----S 116
 135 YKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPQOFIYAGLSALLD 194
 117 KQWDTFUSSELPDWLTATKRGAPDGHAAVAGASQGGYALAAAHFDFRGFAGSLSGFVY 176
 195 PSQGMGPSLIGLAMGDAGGYKAAADMWGPSSDPAMERNDP 233
 177 PSTNYNGAILAGLQFGIDGNGMGAPQLGRWKHDP 215

RESULT 20
 B43603
 antigen 85-C - Mycobacterium bovis (strain BCG) (fragment)
 C:Species: Mycobacterium bovis
 C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 09-Jun-2000
 C:Accession: B43603
 R:Content, J.; de la Cuvelier, A.; De Wit, L.; Vincent-Levy-Frebault, V.; Ooms, J.;
 Infect. Immun. 59, 3205-3212, 1991
 A>Title: The genes coding for the antigen 85-C of Mycobacterium tuberculosis
 n of the gene coding for antigen 85-C of Mycobacterium tuberculosis.
 A:Reference number: A43603; MUID:9134869; PMID:1715324
 A:Accession: B43603
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-57 <CON>
 C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 14.7%; Score 257; DB 2; Length 57;
 Best Local Similarity 88.0%; Pred. No. 3.3e-13;
 Matches 44; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

77 YLLDGLRAODDYNWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPA 126
 1 YLLDGLRAODDYNWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPA 50

RESULT 21
 T29115
 hypothetical protein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
 C:Accession: T29115
 R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: Z17215
 A:Accession: T29115
 A:Status: preliminary; translated from GR/EMBL/DBDUB

A:Molecule type: DNA
A:Residues: 1-342 <PAR>
A:Cross-references: EMBL:AL031350; NID:el316892; PID:el316898; PIDN:CAA20497.1
C:Genetics:
A:Note: SC1P2.06

Query Match
Best Local Similarity 13.4%; Score 233.5; DB 2; Length 342;
Matches 100; Conservative 46; Mismatches 134; Indels 75; Gaps 21;

QY 15 LMIGTAAAVLP-GLVGLAGGAATAGAFSPGLPVEY-----LQVPSPM-GRDI 62
DB LVIALVLLVLTPTAPEALAAAGPETA-TRHGAEVAVTRVADRQVLTVRSALGGRTV 76
QY 63 KVQF--QSGN-----NSPAVLLDGLRAQDDYNGWINTPAFVWYQSLGSLVMPV 112
DB EVRLITPGWPHDRHRHQHPTLLHG--CCGYTSTWSTMDVAETESLSDVLVWPE 134
QY 113 GQGSFYSDWSPACGKAGCQTYKWTFTLSELPQWL-----SANRAVKPTGSAAGLS 166
DB AGWNGWYSDWNH--GQGDPA--WETFTKELRLHRLDRDWGAGNRVV-----AGLS 183
QY 167 MAGSSAMLLAAYHPOF-----IYAGLSALLDPSQMGPSLIGLAMGDAGY--KAADWW 220
DB MGGGALLYAAARHPMFRATAAFSGSAHPLLNDES-----VDRIMGFFAQDNDPLRVW 237
QY 221 GPSSDPA-----WERNDPTQIPLKLVANNTRLVVYCGNGT--PNEELGAN--IPAEP-LE 270
DB G---DPAQRGIWAHDPFHAKRL--RSIPVYLSGDDGTGGLDAPGATSALEADFNQ 292
QY 271 NFVSSNLKFODAYNAAGGHNAVFPPNGPHSHMEYGAQLNAMKGDLSLSLGG 325
DB NHALAAELK-----RVGARVTHTFYCGTHGWAYRERELHSLPMLLGALRVG 341

RESULT 22

D70772
hypothetical protein Rv1288 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: D70772
R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70772
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-456 <COL>
A:Cross-references: GB:273419; GB:AL123456; NID:g3261573; PIDN:CAA97754.1; PID:e243272;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv1288

Query Match
Best Local Similarity 8.4%; Score 146.5; DB 2; Length 456;
Matches 68; Conservative 34; Mismatches 86; Indels 77; Gaps 16;

QY 66 FQSGGNSPAVLLDGLRAQDDYNGWDI-----NTPAFWYQSLGSLVMPVGGQS 117
DB YRTSGRTYFVLYLFGGGTQDFRFDFTGIRDLTAGKP-----IIIVMPDGGHAG 248
QY 118 FYSDWSPACGKAGCQTYKWTFTLSELPQWLSAN--RAVKPTGSAAGLSNAGSSAMTL 175
DB WYSNPSVSPGR-----NWEIFHIAQLPWTLEAFRTVAEYDGRVAGFSMGGFGALKY 303
QY 176 AAYHPCQFIYAGLSALLDPSQMGPSLI-----GL-----AMGDAGGYKAADWWMP 222
DB AAKYGYGHFASASSHS-----GPASLRDRDFGLVHWNALSSAVLDLGG---GTVYGA 351

QY 223 SSDPAWER-----NDPTQIPLKLVANNTRLVVYCGNG-----TPNE---LGGANIPA 266
DB 352 ---PLWDQARVSADNPVERIDSY--RNKFIPLVAGTSPDPANWFDVSNVETQVLQAGOR--- 403
QY 267 EFLNFVRSSNLKF-ODAYNAAGGH 290
DB 404 EFRE---RLSNAGIPHESHEVPGGH 425

RESULT 23

E95071
tributylin esterase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C:Accession: E95071
R;Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei-
nson, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: E95071
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>
A:Cross-references: GB:AB005672; PIDN:AAK74766.1; PID:gl4972089; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0614

Query Match
Best Local Similarity 8.2%; Score 143; DB 2; Length 259;
Matches 66; Conservative 28; Mismatches 104; Indels 46; Gaps 15;

QY 74 PAVYLLDGLRAQDDYNGWINTPAFVWYQSLGSLVMPVGGQSFSYDWYSPACGKAGCQ 133
DB 38 PVLVLLHGM--SGNHSNLARTNVERLLRGTNLIVMP-----NTSGWYTD--QYGF 88
QY 134 TYKWTFTLSELPQWLS---ANRAVPTGSAAGLSNAGSSAMILAAHYHPCQFIYAGSL 190
DB 89 YV---TALABELPQVLKRFPPNMTSKREKTFIAGLSMGYGCFL-ALTNRFSHAASFS 144
QY 191 ALLDPSQMGPSLIGLAMGDAGYKAADWWPSSDPAWERND--PTQIPLKLVANNTRLVW 249
DB 145 GALS-FQNSPESQNL--GSPAYWRG--VGEIRD--WTTPSYLSLESLAKKSKTKLWA 197
QY 250 YCGNGTPELGGANIPAEFL--ENFVRSSNLKFQDAYNAAGGHNAVFPPNGTHSWEY 307
DB 198 WCQE-----QDFLYEANNLAVKNLK-KLGFDTVYSHA-----GTHEWY 237
QY 308 GAQL 311
DB 238 EKQL 241

RESULT 24

C97939
tributylin esterase [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C:Accession: C97939
R;Hoskins, J.A.; Arnold, J.; W.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: C97939
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <KUR>

Fri Feb 6 13:54:47 2004

A;Cross-references: GB:AE007317; PIDN:AAK99343.1; PID:g15458114; GSPDB:GN00174
C;Genetics:
A;Gene: estA

Query Match 8.2%; Score 143; DB 2; Length 259;
Best Local Similarity 27.0%; Pred. No. 0.001;
Matches 66; Conservative 28; Mismatches 104; Indels 46; Gaps 15;

QY 74 PAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSWYSPACGKAGCQ 133
Db 38 PVLVLLHGM--SGNHSWLKKTNVERLLRGTLNIVMP-----NTSNGWYTD--QYGF 88
QY 134 TYKWETFLTSETLPOWLS---ANRAVKPTGSAAGLSVAGSSAMILAAHYHPOOFYAGSL 190
Db 89 YY---TALAELPOLVKRFPPNMTSKREKTFIAGLSMGYGCFL-ALTTRNFSHAASF 144
QY 191 ALLDPSQMGPSLIGLAWDAGGYKAADWGPSSDPAWERN-PTQOIPKLVANNRLIW 249
Db 145 GALS-FQNFSPESQNL--GSPAYWRG--VFGEIRD--WTTSPYSLSLAKSKDKKTLWA 197
QY 250 YCGNGTPELGGANIPAEFL--ENFVRSSNLKFQDAYNAAGHNVAFFNPNGTHSWY 307
Db 198 WCGE-----QDFLYEANNLAVKNLK-KLGFDTVYSHA-----GTHEWY 237
QY 308 GAQL 311
Db 238 EKQL 241

RESULT 25
AB1748
acetyltransferase homolog lin2527 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 19-Apr-2002
C;Accession: AB1748
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC97754.1; PID:g16415049; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2527
C;Superfamily: conserved hypothetical protein YJL068c

Query Match 7.7%; Score 134; DB 2; Length 252;
Best Local Similarity 24.0%; Pred. No. 0.0048;
Matches 61; Conservative 40; Mismatches 85; Indels 68; Gaps 13;

QY 76 VILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYSWYSPACGKAGCQ 135
Db 40 LYILHGL--SNNHTTYVRNTNIERYATEKGLAVIMP--AADHSFYSNMVH---GRDFQ-- 91
QY 136 KWETFLTSETLP-----QWLSANRAVKPTGSAAGLSVAGSSAMILAAHYHPOOFYAGSL 191
Db 92 ----FVSTELPHVMKNWFLPSDKKEDTFIA--GHSMGYGAFAKVALTFPEKFOAASMSG 145
QY 192 LLDPSQMGPSLIGLAWDAGGYKAADWGPSSDPAWERNPTQOIPKLVANNRLWY 251
Db 146 VMDINVIYI-----GGANIPAEF-----LENFVRSSNLKFQDAYNAAGHNVAFFNP 174
QY 252 GNGTPEL-----GGANIPAEF-----LENFVRSSNLKFQDAYNAAGHNVAFFNP 298
Db 175 --GTENDLPHLETLNLTNNVELPALFQNGCTEDFLYEDNLRFRD---FALAKNAPLEYRE 229

QY 299 N-GTHSWEYWGQAQL 311
Db 230 GPGDHDWDFWDKSL 243

RESULT 26

AC1378
acetyltransferase homolog lmo2433 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 02-Aug-2002
C;Accession: A11378
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, H.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: A11378
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAD00511.1; PID:g16411921; GSPDB:GN00177
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2433
C;Superfamily: conserved hypothetical protein YJL068c

Query Match 7.6%; Score 133; DB 2; Length 252;
Best Local Similarity 23.8%; Pred. No. 0.0058;
Matches 61; Conservative 39; Mismatches 76; Indels 80; Gaps 13;

QY 76 VILLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYS-----DWYSPACGK 129
Db 40 LYILHGL--SNNHTTYVRNTNIERYATEKGLAVIMP--AADHSFYSNMVHGRDFE---- 91
QY 130 AGCQTYKWETFLTSETLP-----QWLSANRAVKPTGSAAGLSVAGSSAMILAAHYHPOOFY 185
Db 92 ----FVSTELPHVMKNWFLPSDKKEDTFIA--GHSMGYGAFAKVALTFPEKFOA 139
QY 186 AGSLGALLDPSQMGPSLIGLAWDAGGYKAADWGPSSDPAWERNPTQOIPKLVANN 245
Db 140 AASMSGVMDINVIYI-----KEDCFE--NFSTRITGEMASQT 174
QY 246 RLWVYCGNGTPEL-----GGANIPAEF-----LENFVRSSNLKFQDAYNAAGHN 292
Db 175 ----GTENDLPHLETLNLTNNVELPALFQNGCTEDFLYEDNLRFRD---FALAKNA 223
QY 293 VFNFPN-GTHSWEY 307
Db 224 PLEYREGPGDHDWEP 239

RESULT 27

C86846
lipase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: C86846
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; EhrGenome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A;Reference number: AB6625; MUID:21235186; PMID:11337471
A;Accession: C86846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Cross-references: GB:AE005176; PID:g12724794; PIDN:AAK05869.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yscH

RESULT 29
C41499
alpha-antigen C, extracellular - *Mycobacterium bovis* (fragment)
N; Alternate names: antigen 85A; antigen P32
C; Species: *Mycobacterium bovis*
C; Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jun-2000
C; Accession: C41499; A61471
R; Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990
A; Title: Evidence for three separate genes encoding the proteins of the mycobacterial ar
A; Reference number: A41499; MUID:90093478; PMID:2403534
A; Accession: C41499
A; Status: preliminary

Search completed: February 5, 2004, 17:40:45
Job time : 24.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:25:57 ; Search time 15.4762 Seconds
(without alignments)
987.561 Million cell updates/sec

Title: US-09-805-427A-2
Perfect score: 1745
Sequence: 1 MTDSVRKIRAWRRRLMIGTA.....YWGQQLNMGDLQSSLGAG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127825

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1745	100.0	325	1	A85B MYCTU
2	1706	97.8	323	1	A85B MYCBO
3	1609	92.2	325	1	A85B MYCKA
4	1602	91.8	320	1	A85B MYCSC
5	1539	88.2	330	1	A85B MYCIT
6	1522	87.2	330	1	A85B MYCAV
7	1455	83.4	327	1	A85B MYCLE
8	1425	80.9	347	1	A85A MYCAV
9	1407	80.6	338	1	A85A MYCTU
10	1406	80.6	337	1	A85A MYCUL
11	1383.5	79.3	339	1	A85A MYCGO
12	1338.5	76.7	330	1	A85A MYCLE
13	1198	68.7	340	1	A85C MYCTU
14	1170	67.0	333	1	A85C MYCLE
15	1165	66.8	352	1	A85C MYCAV
16	625	35.8	139	1	A85A MYCMR
17	519	29.7	299	1	MP51 MYCTU
18	498.5	28.6	301	1	MP75 MYCLE
19	470	26.9	657	1	CSP1 CORGL
20	146.5	8.4	456	1	YC88 MYCTU
21	125	7.2	282	1	ESTD HUMAN
22	116	6.6	458	1	AGLE RHIME
23	109	6.2	827	1	XANP YANS2
24	106	6.1	414	1	PHAI PSELE
25	102	5.8	1106	1	GLI1 HUMAN
26	101	5.8	344	1	TOR2 HUMAN
27	100.5	5.8	426	1	Y967 CORGL
28	100	5.7	416	1	CBPB CANFA
29	99.5	5.7	555	1	WEPA EWENT
30	97.5	5.6	277	1	YAIM ECOLI
31	97.5	5.6	2364	1	PGCA BOVIN
32	97	5.6	264	1	GUNS BRWCA
33	95.5	5.5	440	1	PORP_PSEAE

RESULT 1

ID	A85B MYCTU	STANDARD;	PRT;	325 AA.
AC	P31952; Q9RM10;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85 complex B) (Ag85B) (Mycobyl transferase 85B) (EC 2.3.1.-)			
DE	(Fibronectin-binding protein B) (30 kDa extracellular protein).			
GN	FBPB OR RV1886C OR MT1934 OR MTCY180.32.			

ALIGNMENTS

34	95.5	5.5	488	1	PHB ALCEFA
35	93.5	5.4	473	1	Y333 MYCLE
36	92.5	5.3	345	1	Y032 MOUSE
37	91.5	5.2	299	1	Y038 YEAST
38	91.5	5.2	403	1	H136 ARATH
39	90.5	5.2	458	1	BPHA PSEFS
40	90.5	5.2	538	1	TCMA STRGA
41	90	5.2	563	1	IDS MOUSE
42	90	5.2	1101	1	GUNC CELFI
43	89	5.1	311	1	ISPE SYNEL
44	88.5	5.1	639	1	EY44 HUMAN
45	88	5.0	228	1	CE21 PEA
46	88	5.0	424	1	GUN1 RALSO
47	87	5.0	236	1	TENA BACSU
48	86.5	5.0	263	1	CB23 SOYEN
49	86	4.9	334	1	E13B HORVU
50	86	4.9	374	1	ADH3 KLULA
51	85.5	4.9	600	1	LAM2 HUMAN
52	85	4.9	299	1	YHXD BACSU
53	85	4.9	353	1	FAEB PENFN
54	84.5	4.8	268	1	CB28 PEA
55	84.5	4.8	339	1	DUSC MOUSE
56	84.5	4.8	444	1	RUMA XANCP
57	84.5	4.8	473	1	Y333 MYCTU
58	84.5	4.8	521	1	LAG3 MOUSE
59	84.5	4.8	901	1	A180 MOUSE
60	84.5	4.8	997	1	ATS7 HUMAN
61	84.5	4.8	1070	1	EMBC MYCLE
62	84	4.8	580	1	PTFB XANCP
63	84	4.8	725	1	GUNG CLOCE
64	84	4.8	864	1	ELS RAT
65	84	4.8	1123	1	V120 HSV11
66	83.5	4.8	511	1	GUNB_PSEFL
67	83.5	4.8	540	1	Y8M YEAST
68	83.5	4.8	1433	1	SUBF BACSU
69	83	4.8	269	1	CB22 PEA
70	83	4.8	361	1	PAX1 MOUSE
71	83	4.8	458	1	BPHA BURCE
72	83	4.8	474	1	SOXA HUMAN
73	83	4.8	700	1	PURL HALN1
74	83	4.8	1134	1	YML7 YEAST
75	82.5	4.7	500	1	AMPA CORGL
76	82.5	4.7	548	1	LAC1 PHLRA
77	82.5	4.7	722	1	GUNF CLOCE
78	82.5	4.7	1032	1	EMBA MYCSM
79	82	4.7	674	1	YL10 VIBCH
80	82	4.7	757	1	DHET GLDOX
81	82	4.7	860	1	ELS MOUSE
82	82	4.7	1365	1	KRES YEAST
83	82	4.7	3119	1	CAIC MOUSE
84	81.5	4.7	278	1	YEIG ECOLI
85	81.5	4.7	313	1	EBAG STRPL
86	81.5	4.7	345	1	ESTA STRSC
87	81.5	4.7	420	1	PEL BACSU
88	81.5	4.7	466	1	HYIN AGRRH
89	81.5	4.7	527	1	YF00 MYCPN
90	81.5	4.7	1654	1	OMP_PICRI

P12625	alcaligenes
P37391	mycobacteri
Q9JMS5	mus musculu
P40363	saccharomyc
O82660	arabidopsi
Q52028	pseudomonas
P39886	streptomyce
O08890	mus musculu
P14090	cellulomona
Q8DJ11	synechococ
O95677	homo sapien
P04159	pisum sativ
P58599	raistonia s
P25052	bacillus su
P09756	glycine max
P15737	hordeum vul
P49384	kluyveromyc
Q9HE18	penicillium
P27490	pisum sativ
Q9D0T2	mus musculu
Q8PB48	xanthomonas
O06250	mycobacteri
O61790	mus musculu
Q61548	mus musculu
Q9UKP4	homo sapien
Q9CDA7	mycobacteri
P23355	xanthomonas
P37700	clostridium
Q99372	rattus norv
P10221	herpes simp
P18126	pseudomonas
Q03263	saccharomyc
P16397	bacillus su
P07371	pisum sativ
P09084	mus musculu
P37333	burkholderi
Q06945	homo sapien
Q9HR49	halobacteri
Q03735	saccharomyc
Q8NN14	corynebacte
O01679	phlebia rad
P37698	clostridium
Q50394	mycobacteri
Q9KG91	vibriol chol
O05542	gluconobact
P54320	mus musculu
P22023	saccharomyc
Q06847	mus musculu
P33018	escherichia
P04067	streptomyce
P22266	streptomyce
P39116	bacillus su
Q09102	agrobacteri
P75287	mycoplasma
Q53047	r outer mem

OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Erddmann;
RX MEDLINE=95078461; PubMed=7987013;
RA de Wit L., Palou M., Content J.;
RT "Nucleotide sequence of the 85B-protein gene of Mycobacterium bovis
RT BCG and Mycobacterium tuberculosis.";
RL DNA Seq. 4:267-270(1994).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Erddmann;
RX MEDLINE=96333337; PubMed=8757831;
RA Harth G., Lee B.Y., Wang J., Clemens D.L., Horwitz M.A.;
RT "Novel insights into the genetics, biochemistry, and
RT immunocytochemistry of the 30-kilodalton major extracellular protein
RT of Mycobacterium tuberculosis.";
RL Infect. Immun. 64:3038-3047(1996).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.B. III, Tekaa F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.F., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE OF 41-325 FROM N.A.
RC STRAIN=ATCC 201 / H37Ra;
RA Fan X.L., Xu Z.H.K., Bai G.C.H., Li Y.;
RT "Cloning and construction of a eukaryotic expression vector containing
RT Ag85B gene of Mycobacterium tuberculosis.";
RL J. Mol. Cell. Immunol. 0:0-0(2000).
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM F51 PROTEIN.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; X62398; CAA44269.1; -;
CC EMBL; U38939; AAC44294.1; -;

DR EMBL; Z97193; CAB10044.1; -;
DR EMBL; AEO07049; AAK46207.1; ALT_INT.
DR EMBL; AF198032; AAF13448.1; -;
DR PR; C70516; C70516
DR PDB; 1FON; 28-MAR-01.
DR PDB; 1FOP; 28-MAR-01.
DR TIGR; MT1934; -;
DR TubercuList; Rv1886c; -;
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Antigen; Signal; Complete proteome;
KW 3D-structure.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 325 ANTIGEN 85-B.
FT ACT_SITE 166 166 BY SIMILARITY.
FT ACT_SITE 270 270 BY SIMILARITY.
FT ACT_SITE 302 302 BY SIMILARITY.
SQ SEQUENCE 325 AA; B993B5442FD5567D CRC64;
Query Match 100.0%; Score 1745; DB 1; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.3e-124;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAAGTAAGAFRRPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAAGTAAGAFRRPGLPVEYLQVPSMGR 60
QY 61 DIKQVQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSPYS 120
DB 61 DIKQVQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSPYS 120
QY 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
DB 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QQFIYAGSLALLDPSQGMPSLIGLAMDAGGYKAADWGPSSDPAMERNPTQIIPKL 240
DB 181 QQFIYAGSLALLDPSQGMPSLIGLAMDAGGYKAADWGPSSDPAMERNPTQIIPKL 240
QY 241 VANNTRLMVYCGNGTPNELGGANI PAEFLNFVRSNLFKFDAYNAAGSHNAVFNPFPNG 300
DB 241 VANNTRLMVYCGNGTPNELGGANI PAEFLNFVRSNLFKFDAYNAAGSHNAVFNPFPNG 300
QY 301 THSWEYGAQLNAMKGDQLQSSLGAG 325
DB 301 THSWEYGAQLNAMKGDQLQSSLGAG 325
RESULT 2
A85B MYCBO STANDARD; PRT; 323 AA.
ID A35E MYCBO
AC P12542;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
DE complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
DE (Fibronectin-binding protein B).
GN FBPP.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 41-70.
RC STRAIN=BCG;
RX MEDLINE=88314872; PubMed=2842287;
RA Matsuo K., Yamaguchi R., Yamazaki A., Tasaka H., Yamada T.;
RT "Cloning and expression of the Mycobacterium bovis BCG gene for
RT extracellular alpha antigen.";
RL J. Bacteriol. 170:3847-3854(1988).
[2]
RN SEQUENCE FROM N.A.

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RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=95078461; PubMed=7987013;
RA de Wit L., Palcou M., Content J.;
RT "Nucleotide sequence of the 85B-protein gene of Mycobacterium bovis
RL BCG and Mycobacterium tuberculosis.";
RL DNA Seq. 4,267-270(1994).
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYLTTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM PS1 PROTEIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M21839; AAA25359.1; -.
CC DR EMBL; X62397; CAA44268.1; -.
CC DR PIR; A32348; A32348.
CC DR PIR; S29663; S29663.
CC DR HSSP; P31953; 1DOY.
CC DR InterPro; IPR000801; Esterase_put.
CC DR Pfam; PF00756; Esterase; 1.
CC KW Transferase; Acyltransferase; Antigen; Signal.
CC FT SIGNAL 1 40
CC FT CHAIN 41 323 ANTIGEN 85-B.
CC FT ACT_SITE 166 166 BY SIMILARITY.
CC FT ACT_SITE 268 268 BY SIMILARITY.
CC FT ACT_SITE 300 300 BY SIMILARITY.
CC FT CONFLICT 200 200 G -> GPS (IN REF. 2).
CC FT CONFLICT 283 284 KP -> NA (IN REF. 2).
CC SQ SEQUENCE 323 AA; 34403 MW; 26C2A1BFID0464BA CRC64;

Query Match 97.8%; Score 1706; DB 1; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.2e-121;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAALIGLSMAGSSAMILAAYHP 180
Db 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAALIGLSMAGSSAMILAAYHP 180
QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPANERNPTQOIPKL 240
Db 181 QOPIYAGLSALLDPSQGMG--LIGLAMDAGGYKAADMWGPSSDPANERNPTQOIPKL 238
QY 241 VANNTRLWYCGNGTNPENELGGANI PAEFLNFVRSSNLKFQDAYNAAGHNAVFNPFG 300
Db 239 VANNTRLWYCGNGTNPENELGGANI PAEFLNFVRSSNLKFQDAYNAAGHNAVFNPFG 298
QY 301 THSWYWGQALNMGKDIOSSILGAG 325
Db 299 THSWYWGQALNMGKDIOSSILGAG 323

RESULT 3
A85B MYCKA
ID A85B MYCKA STANDARD; PRT; 325 AA.
AC P211160;

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DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
DE complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
DE (Fibronectin-binding protein B).
DE FBPB.
GN Mycobacterium kansasii.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1768;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=90129315; PubMed=2404875;
RA Matsuo K., Yamaguchi R., Yamazaki A., Tasaka H., Terasaka K.,
RA Yamada T.;
RT "Cloning and expression of the gene for the cross-reactive alpha
RT antigen of Mycobacterium kansasii.";
RL Infect. Immun. 58:550-556(1990).
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYLTTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM PS1 PROTEIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X53897; CAA37868.1; -.
CC DR PIR; A37185; A37185.
CC DR HSSP; P31953; 1DOY.
CC DR InterPro; IPR000801; Esterase_put.
CC DR Pfam; PF00756; Esterase; 1.
CC KW Transferase; Acyltransferase; Antigen; Signal.
CC FT SIGNAL 1 40
CC FT CHAIN 41 325 ANTIGEN 85-B.
CC FT ACT_SITE 166 166 BY SIMILARITY.
CC FT ACT_SITE 270 270 BY SIMILARITY.
CC FT ACT_SITE 302 302 BY SIMILARITY.
CC SQ SEQUENCE 325 AA; 34323 MW; 5F2281BCC48AE30D CRC64;

Query Match 92.2%; Score 1609; DB 1; Length 325;
Best Local Similarity 89.8%; Pred. No. 2.4e-114;
Matches 291; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSKIRAWGRRLLVGAAAALPGLVGLAGGATAGAFSRPGLPVEYLQVPSAAGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 61 SIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
QY 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAALIGLSMAGSSAMILAAYHP 180
Db 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAALIGLSMAGSSAMILAAYHP 180
QY 181 QOPIYAGLSALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPANERNPTQOIPKL 240
Db 181 QOPIYAGLSALLMDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPANERNPTQOIPKL 240
QY 241 VANNTRLWYCGNGTNPENELGGANI PAEFLNFVRSSNLKFQDAYNAAGHNAVFNPFG 300
Db 241 VANNTRLWYCGNGTNPENELGGANVPAEFLNFVRSSNLKFQDAYNAAGHNAVFNDANG 300

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181 QQFIYAGSLALDPSQGMGSLIIGLAMDAGYKADWGPSSDPARWENDETQIIPKL 240
 181 QQFIYAGSLALDPSQGMGSLIIGLAMDAGYKADWGPSSDPARWENDETQIIPKL 240
 241 VANNRLWYCGNGTNEELGGANIPEEFLENVRSSNLKFQDAYNAGGHNAVFNPFPNG 300
 241 VGNTRLWYCGNGTPELGGANPAEFLENFVRSSNLKFQDAYNAGGHNAVFHPDNG 300
 301 THSWEYGAOLNNAKMDGLQSSLGA 324
 301 THSWEYGAOLNNAKMDLQTLGA 324

RESULT 5

AS8B_MYCIT STANDARD; PRT; 330 AA.
 ID AS8B_MYCIT
 AC Q49575; P94938;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85 complex B) (Ag85B) (Mycobyl transferase 85B) (EC 2.3.1.-)
 DE (Fibronectin-binding protein B).
 DE FEPPB.
 GN Mycobacterium intracellulare.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1767;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13950;
 RX MEDLINE=94071912; PubMed=8250904;
 RA Kitaura H., Ohara N., Matsuo T., Tasaka H., Kobayashi K., Yamada T.;
 RT "Cloning, sequencing and expression of the gene for alpha antigen from Mycobacterium intracellulare and use of PCR for the rapid identification of Mycobacterium intracellulare";
 RT Biochem. Biophys. Res. Commun. 196:1466-1473(1993).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.

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EMBL; D16546; BAA03981.1; -;
 EMBL; D14253; BAA03243.1; -;
 PIR; JN0897; JN0897.
 HSP; P31953; 1DQY.
 InterPro; IPR00801; Esterase_put.
 Pfam; PF00756; Esterase; 1.
 Transferase; Acyltransferase; Antigen; Signal.
 SIGNAL 1 40 BY SIMILARITY.
 CHAIN 41 330 ANTIGEN 85-B.
 FT ACT_SITE 166 166 BY SIMILARITY.
 FT ACT_SITE 270 270 BY SIMILARITY.
 FT ACT_SITE 302 302 BY SIMILARITY.
 FT ACT_SITE 310 310 Q -> S (IN REF. 1; BAA03243).
 FT CONFLICT 310 310 Q -> S (IN REF. 1; BAA03243).
 FT CONFLICT 310 310 Q -> S (IN REF. 1; BAA03243).
 SQ SEQUENCE 330 AA; 34507 MW; 83090670FABAE0D5 CRC64;

Query Match 88.2%; Score 1539; DB 1; Length 330;
 Best Local Similarity 85.8%; Pred. No. 4.6e-109;
 Matches 278; Conservative 23; Mismatches 23; Indels 0; Gaps 0;

301 THSWEYGAOLNNAKMDGLQSSLGA 324
 301 THSWEYGAOLNNAKMDLQTLGA 324

RESULT 4

AS8B_MYCSC STANDARD; PRT; 330 AA.
 ID AS8B_MYCSC
 AC Q50397;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85 complex B) (Ag85B) (Mycobyl transferase 85B) (EC 2.3.1.-)
 DE (Fibronectin-binding protein B).
 DE FEPPB.
 GN Mycobacterium scrofulaceum.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19981;
 RX MEDLINE=94323707; PubMed=8047837;
 RA Takano M., Ohara N., Mizuno A., Yamada T.;
 RT "Cloning, sequencing and expression in Escherichia coli of the gene for alpha antigen from Mycobacterium scrofulaceum";
 RT Scand. J. Immunol. 40:165-170(1994).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.

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EMBL; D26187; BAA05332.1; -;
 HSP; P31953; 1DQY.
 InterPro; IPR00801; Esterase_put.
 Pfam; PF00756; Esterase; 1.
 Transferase; Acyltransferase; Antigen; Signal.
 SIGNAL 1 40 BY SIMILARITY.
 CHAIN 41 330 ANTIGEN 85-B.
 FT ACT_SITE 166 166 BY SIMILARITY.
 FT ACT_SITE 270 270 BY SIMILARITY.
 FT ACT_SITE 302 302 BY SIMILARITY.
 SQ SEQUENCE 330 AA; 34943 MW; 09D6E04B5E9ED221 CRC64;

Query Match 91.8%; Score 1602; DB 1; Length 330;
 Best Local Similarity 89.5%; Pred. No. 8.2e-114;
 Matches 290; Conservative 22; Mismatches 12; Indels 0; Gaps 0;

1 MTDSVKIRAWGRRLMTGTAANVVLPGVLGAGATAGAFSRPLVEYLQVPSMGR 60
 1 MTDSVKIRAWGRRLMTGTAANVVLPGVLGAGATAGAFSRPLVEYLQVPSMGR 60
 61 DIKVOFGSGNNSPAVLLDGLRAQDDYNGWDINTPAFWYQSLGSLIVPVGQSSFFYS 120
 61 DIKVOFGSGNNSPAVLLDGLRAQDDYNGWDINTPAFWYQSLGSLIVPVGQSSFFYS 120
 121 DWYSPACGKAGCTYKWTFTLSELTPQLWLSANRAVKPTGSAIIGLSWAGSAMLIAYHP 180
 121 DWYSPACGKAGCTYKWTFTLSELTPQLWLSANRAVKPTGSAIIGLSWAGSAMLIAYHP 180


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QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTDISEKVRWGRRLVVGAAAATLPGVLGAGGAATANAFSRPGLPVEYLQVPSAGMR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DIKVOFGSGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSVMPVGGSSFFS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DIKVOFGSGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSVMPVGGSSFFA 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 DWYSPACGKACGCTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 DWYQPCGKAGCSTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAVNHP 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 QQFIYAGLSALLDPSQGMPSLIGLAMDAGGYKADAMWGPSSDPDAWERNPTQQIPKL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 NQFIYAGLSALLDPSQGMPSLIGLAMDAGGYKADAMWGPSSDPDAWQNDPSLQIPAL 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VANNTRLVWYCGNGTNPGLGAGNIPAEFLENFVRSSNLKFQDAYNAAGHNAVFENPANG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VGNTRLWYCGNGTNPSELGGANPAEFLENFVRSSNLKFQDAYNAAGHNAVFENFANG 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 THSWEYWGAGLNAMKPDQLQSLGA 324
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 THSWEYWGAGLNAMKPDQLQSLGA 324
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 6

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A85B_MYCAV STANDARD; PRT; 330 AA.
AC Q06947;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
DE complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
DE (Fibronectin-binding protein B).
GN FBPB.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93202712; PubMed=7681039;
RA Ohara N., Matsuo K., Yamaguchi R., Yamazaki A., Tasaka H.,
RA Yamada T.;
RT "Cloning and sequencing of the gene for alpha antigen from
RT Mycobacterium avium and mapping of B-cell epitopes.";
RL Infect. Immun. 61:1173-1179(1993).
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYLTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM PSI PROTEIN.
CC [2]

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DR EMBL; X63437; CAA45032.1; -.
DR HSSP; P31953; 1DOY.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Antigen; Signal.
FT SIGNAL 1 40 BY SIMILARITY.
FT CHAIN 41 330 ANTIGEN 85-B.

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FT ACT SITE 166 166 BY SIMILARITY.
FT ACT SITE 270 270 BY SIMILARITY.
FT ACT SITE 302 302 BY SIMILARITY.
SQ SEQUENCE 330 AA; 34734 MW; 6ACAS980B840B2D8 CRC64;

Query Match 87.2%; Score 1522; DB 1; Length 330;
Best Local Similarity 84.9%; Pred. No. 8.8e-108;
Matches 275; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDISEKVRWGRRLVVGAAAATLPGVLGAGGAATANAFSRPGLPVEYLQVPSAGMR 60
QY 61 DIKVOFGSGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSVMPVGGSSFFS 120
Db 61 DIKVOFGSGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSVMPVGGSSFFA 120
QY 121 DWYSPACGKACGCTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
Db 121 DWYQPCGKAGCSTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAVNHP 180
QY 181 QQFIYAGLSALLDPSQGMPSLIGLAMDAGGYKADAMWGPSSDPDAWERNPTQQIPKL 240
Db 181 DQFIYAGLSALLDPSQGMPSLIGLAMDAGGYKADAMWGPSSDPDAWQNDPSLHIPEL 240
QY 241 VANNTRLVWYCGNGTNPGLGAGNIPAEFLENFVRSSNLKFQDAYNAAGHNAVFENPANG 300
Db 241 VGNTRLWYCGNGTNPSELGGANPAEFLENFVRSSNLKFQDAYNAAGHNAVFENFANG 300
QY 301 THSWEYWGAGLNAMKPDQLQSLGA 324
Db 301 THSWEYWGAGLNAMKPDQLQSLGA 324

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RESULT 7

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A85B_MYCLE STANDARD; PRT; 327 AA.
AC P31951; Q9RIA5;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85
DE complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)
DE (Fibronectin-binding protein B).
GN FBPB OR ML2028 OR MLCB561.03C.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92051335; PubMed=1945958;
RA de Mendonca Lima L., Content J., van Heuverswyn H., Degraeve W.;
RT "Nucleotide sequence of the gene coding for the 85-B antigen of
RT Mycobacterium leprae.";
RL Nucleic Acids Res. 19:5789-5789(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN:TN;
RC MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A

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CC MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.
CC
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CC
CC -----
CC EMBL; X60934; CAA43269.1; --
CC DR EMBL; AL049571; CAB40285.1; --
CC DR EMBL; AL583924; CAC30983.1; --
CC DR FJ; G87162; G87162.
CC DR FJ; S34434; S34434.
CC DR HSP; F31953; 1DQY.
CC DR Leproma; ML2028; --
CC DR InterPro; IPR000801; Esterase_put.
CC DR Pfam; PF00756; Esterase; 1.
CC KW Transferase; Acyltransferase; Antigen; Signal; Complete proteome.
CC FT SIGNAL 1 38 POTENTIAL.
CC FT CHAIN 39 327 ANTIGEN 85-B.
CC FT ACT SITE 164 164 BY SIMILARITY.
CC FT ACT SITE 268 268 BY SIMILARITY.
CC FT ACT SITE 300 300 BY SIMILARITY.
CC FT CONFLICT 59 59 S -> T (IN REF. 1).
CC SQ SEQUENCE 327 AA; 34807 MW; 2B0EB9B37A0F985C CRC64;

Query Match 83.4%; Score 1455; DB 1; Length 327;
Best Local Similarity 83.0%; Pred. No. 9.9e-103;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MTDVSRKTRNGRRIMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
DB 1 MIDVSGKIRAWGRWLVG--AAATPLSLISLAGGAATASAFSRPGLPVEYLQVPSMGR 58

QY 61 DIKVOFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFY 120
DB 59 SIKVOFQGGNGSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSSFY 118

QY 121 DWYSPACGKAGCQTYKWTFTLSELPQWLANSRAVKTGSAAGLSMAGSSAMILAAVHP 180
DB 119 DWYSPACGKAGCQTYKWTFTLSELPQWLANSRVKSTGSAVVGSLMAGSSALILAAVHP 178

QY 181 QQFIYAGLSALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDPAMERNPTQIQI 240
DB 179 DQFIYAGLSALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDPAMERNPTQIQI 238

QY 241 VANNTHLWYVCGNGTPELGGANI PAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 300
DB 239 VANNTHLWYVCGNGTPELGGNI PAEFLNFVRSSNLKFDAYNAAGGHNAVFPPNG 298

QY 301 THSWYEWGAQLNAMKGDQLQSSLGA 324
DB 299 THSWYEWGAQLNAMKPDQLQNTLMA 322

RESULT 8
A85A MYCAV STANDARD; PRT; 347 AA.
ID A85A MYCAV
AC O52956;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A) (Mycoly 1
GN transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A).
OS Mycobacterium avium.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97427949; PubMed=9284137;
RA Ohara N., Ohara-Wada N., Kitaura H., Nishiyama T., Matsumoto S.,
RA Yamada T.;
RA "Analysis of the genes encoding the antigen 85 complex and MP751 from
RT Mycobacterium avium";
RL Infect. Immun. 65:3680-3685 (1997).
CC -1- FUNCTION: PROTEIN OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- PFM: CONTAINS ONE DISULFIDE BRIDGE (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.
CC
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CC
CC -----
CC EMBL; D78144; BAA24156.1; --
CC DR HSP; F31953; 1DQY.
CC DR InterPro; IPR000801; Esterase_put.
CC DR Pfam; PF00756; Esterase; 1.
CC KW Transferase; Acyltransferase; Signal; Antigen.
CC FT SIGNAL 1 43 POTENTIAL.
CC FT CHAIN 44 347 ANTIGEN 85-A.
CC FT ACT SITE 169 169 BY SIMILARITY.
CC FT ACT SITE 273 273 BY SIMILARITY.
CC FT ACT SITE 305 305 BY SIMILARITY.
CC SQ SEQUENCE 347 AA; 36095 MW; DFAFF3DE504C208E CRC64;

Query Match 80.9%; Score 1412.5; DB 1; Length 347;
Best Local Similarity 78.9%; Pred. No. 1.7e-99;
Matches 258; Conservative 26; Mismatches 40; Indels 3; Gaps 1;

QY 1 MTDVSR---KIRAWGRRIMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPS 57
DB 1 MTLVDRLRGAVAGMPRRLLVVGAGAGALLSGLIGAVGSSATAGAFSRPGLPVEYLQVPSAA 60

QY 58 MGRDVKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSS 117
DB 61 MGRDVKVQFQSGGNSPALYLLDGMRAQDDFNGWDINTPAFEWYQSGISVAMPVGGQSS 120

QY 118 FYSDWYSPACGKAGCQTYKWTFTLSELPQWLANSRAVKTGSAAGLSMAGSSAMILAA 177
DB 121 FYSDWYKPCACGKAGCQTYKWTFTLSELPQYLSAQKQVKPTGSGVVGSLMAGSSAILAA 180

QY 178 YHPQOFIYAGLSALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDPAMERNPTQIQI 237
DB 181 YHPDQFVYAGLSALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDPAMERNPTQIQI 240

QY 238 PKLVANNTRIMVYVCGNGTPELGGANI PAEFLNFVRSSNLKFDAYNAAGGHNAVFPP 297
DB 241 GKLVANNTRIMVYVCGNGKPSDLGGNLPKAFLEGEFVRTSNLKFQDAYNGAGGHNAVF 300

QY 298 PNGTHSWYEWGAQLNAMKGDQLQSSLGA 324
DB 301 ANGTHDWPYWGALQAMKPDQLQSVIGA 327

RESULT 9
A85A MYCTU STANDARD; PRT; 338 AA.
ID A85A MYCTU

AC P17944; P17996;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A) (Mycoly1
 DE transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A).
 GN FBPA OR MP744 OR RV3804C OR MT3911 OR MT026.09C.
 OS Mycobacterium tuberculosis, and
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
 RX MEDLINE=9633337; PubMed=2506131;
 RA Borremans M., de Wit L., Volckart G., Ooms J., de Bruyn J.,
 RA Huygen K., van Vooren J.P., Stelander M., Verhofstad R., Content J.,
 RT "Cloning, sequence determination, and expression of a 32-kilodalton-
 RT protein gene of Mycobacterium tuberculosis";
 RL Infect. Immun. 57:3123-3130(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=Erdmann;
 RX MEDLINE=9633337; PubMed=8757831;
 RA Harth G., Lee B.Y., Wang J., Clemens D.L., Horwitz M.A.;
 RL Infect. Immun. 65:852-852(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagers K., Krogh A., McLean L.A., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence";
 RL Nature 393:537-544(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Emdolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=M.bovis; STRAIN=BCG / Paris 1173 P2;
 RX MEDLINE=90326531; PubMed=2197602;
 RA de Wit L., de la Cuvelier A., Ooms J., Content J.;
 RT "Nucleotide sequence of the 32 kDa-protein gene (antigen 85 A) of
 RT Mycobacterium bovis BCG";
 RL Nucleic Acids Res. 18:3995-3995(1990).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
 CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
 CC MYCOLYLTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
 CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
 CC FOR MAINTAINING CELL WALL INTEGRITY.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: CONTAINS ONE DISULFIDE BRIDGE.
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
 CC N-TERMINAL OF C. GLUTAMICUM PSI PROTEIN.
 CC
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 CC
 CC EMBL; M27016; AAA50288.1; ALT_SEQ.
 CC EMBL; U47335; AAC44295.1; -;
 CC EMBL; AL022076; CAA17868.1; -;
 CC EMBL; AE007185; AAK48277.1; ALT_INIT.
 CC EMBL; D26486; BAA05496.1; -;
 CC EMBL; X53034; CAA37206.1; -;
 CC PIR; H70887; H70887.
 CC PIR; S10326; S10326.
 CC HSP; P31953; 1DQY.
 CC TIGR; MT3911; -;
 CC Tuberculin; RV3804C; -;
 CC InterPro; IPR000801; Esterase_put.
 CC Pfam; PF00756; Esterase; 1.
 KW Transferase; Acyltransferase; Signal; Antigen; Complete proteome.
 FT SIGNAL 1 42
 FT CHAIN 43 338 ANTIGEN 85-A.
 FT ACT_SITE 169 169 BY SIMILARITY.
 FT ACT_SITE 273 273 BY SIMILARITY.
 FT ACT_SITE 305 305 BY SIMILARITY.
 FT CONFLICT 24 26 GAA -> AR (IN REF. 1).
 FT CONFLICT 131 131 G -> R (IN REF. 1).
 FT CONFLICT 292 292 G -> R (IN REF. 1).
 FT CONFLICT 324 334 ALGATNTGPA -> HWVPRTPGP (IN REF. 1).
 FT SEQUENCE 338 AA; 35686 MW; 57B1CF95D07D52C0 CRC64;
 Query Match 80.6%; Score 1407; DB 1; Length 338;
 Best Local Similarity 78.9%; Pred. No. 4.3e-99;
 Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;
 QY 8 IRAGRLMTIGTAAAVLVGLVGLAGGAAATAGAFSPRLPVEYLQVPSMGRDIKVFQ 67
 DB 11 VTGMSRLVVGAVGAALVSLVGLVAGVGTATAGAFSPRLPVEYLQVPSMGRDIKVFQ 70
 QY 68 SGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSLSVMPVGGQSSFYSDWSPAC 127
 DB 71 SGGNSPALYLLDGLRAQDDYNGWDINTPAFEWYQSLSVMPVGGQSSFYSDWSPAC 130
 QY 128 GKAGCQTYKWEFTLTSELPQWLSANRAVKPTGSAALGLSWAGSSAMILAAHYHPQOFTYAG 187
 DB 131 GKAGCQTYKWEFTLTSELPQWLSANRAVKPTGSAALGLSWAGSSAMILAAHYHPQOFTYAG 190
 QY 188 SLSALLDPQGMGSPSLIGLWAGDAGGYKAADMMWGPSSDPWENDPTQIPLKLVANTR 247
 DB 191 AMSGLDPSQMGPTLLIGLWAGDAGGYKASDMMWGPSSDPWENDPTQIPLKLVANTR 250
 QY 248 WYCGNGTNPGLGANIPAEFLNFVRSSNLKFQDAYNAGGHNVAFNFPNCTHSEWY 307
 DB 251 WYCGNGKPSDLGGNNLPKFLFEGFVRTSNIRKFDAYNAGGHNVAFNFPNCTHSEWY 310
 QY 308 GAQLNMGKDLQSSIGA 324
 DB 311 GAQLNMGKDLQSSIGA 327
 RESULT 10
 A85A_MYCUL
 ID A85A_MYCUL STANDARD; PRT; 337 AA.
 AC P58248;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A) (Mycoly1
DE transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A).
GN FBPA.
OS Mycobacterium ulcerans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1909;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ITM 5150;
RA Ianghe A.J.;
RT "Protective efficacy of DNA vaccine encoding antigen 85A from M. bovis
RT BCG against Buruli Ulcer.";
RL Thesis (2001), Universite Libre de Bruxelles, Belgium.
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PTM: CONTAINS ONE DISULFIDE BRIDGE (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C.GLUTAMICUM PSI PROTEIN.
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CC -----
DR EMBL; AJ300576; CAC40861.1; -.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Signal; Antigen.
FT SIGNAL 1 42 BY SIMILARITY.
FT CHAIN 43 337 ANTIGEN 85-A.
FT ACT_SITE 169 169 BY SIMILARITY.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 305 305 BY SIMILARITY.
SQ SEQUENCE 337 AA; 35643 MW; 99022B84077E5773 CRC64;

Query Match 80.6%; Score 1406; DB 1; Length 337;
Best Local Similarity 80.4%; Pred. No. 5e-99;
Matches 251; Conservative 31; Mismatches 30; Indels 0; Gaps 0;

QY 13 RLIMIGTAAAVLPGLVGLAGGAATAGAFSPRLPVEYLQVPSMGRDIKVFQSGGNN 72
DB 16 RLIMVGAAGVALLSLGLVGVGGATASAFSPRLPVEYLQVPSMGRNIKVFQSGGAN 75

QY 73 SPAYLLDGLRAODDNGWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPACGKAGC 132
DB 76 SPAYLLDGMRAODDNGWDINTPAFEWYQSGISVAMPVGGSSFYSDWYSPACGKAGC 135

QY 133 QTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPDQFVYAGLSAL 192
DB 136 TTYKWTFTLSELPAVLASNKQVKPTGSAAGLSMAGSSAMILAAVHPDQFVYAGLSAL 195

QY 193 LDPDSQMGPSLIGLAMGDAGGYKADWGPSPDPAWRNDPTQIQPKLVANNTLWYCG 252
DB 196 LDPDSQMGPSLIGLAMGDAGGYKADWGPSPDPAWRNDPTQIQPKLVANNTLWYCG 255

QY 253 NGTPNELGGANI PAEFLNENFVRSSNLKFQDAYNAAGHNAVFPNPNNGTHSWYWGQALN 312
DB 256 NGKPSDLGGDNLPAKFLGFGVFTSTNMFQAAAYNAAGHNAVFPNPNNGTHSWYWGQALN 315

QY 313 AMKGDQLQSSILGA 324
DB 316 AMRPDLQTLGA 327

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RESULT 11
A85A_MYCGO STANDARD; PRT; 339 AA.
AC Q060E2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A) (Mycoly1
DE transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A).
GN FBPA.
OS Mycobacterium gordonae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1778;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14470;
RA Dumonceaux M.; Fauville-Dufaux M.; Ooms J.; de Wit L.; Content J.;
RT "Cloning and sequencing of the 85A antigen from Mycobacterium
RT gordonae and its use for the specific PCR identification of these
RT mycobacteria.";
RT MYCOLYTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
RT TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
RT FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: CONTAINS ONE DISULFIDE BRIDGE (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C.GLUTAMICUM PSI PROTEIN.
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CC -----
DR EMBL; Y10378; CAA71406.1; -.
DR HSP; P31953; IDQY.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Transferase; Acyltransferase; Signal; Antigen.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 44 339 ANTIGEN 85-A.
FT ACT_SITE 169 169 BY SIMILARITY.
FT ACT_SITE 272 272 BY SIMILARITY.
FT ACT_SITE 304 304 BY SIMILARITY.
SQ SEQUENCE 339 AA; 35474 MW; 909B7E0E3969E2DE CRC64;

Query Match 79.3%; Score 1383.5; DB 1; Length 339;
Best Local Similarity 79.5%; Pred. No. 2.5e-97;
Matches 248; Conservative 33; Mismatches 30; Indels 1; Gaps 1;

QY 13 RLIMIGTAAAVLPGLVGLAGGAATAGAFSPRLPVEYLQVPSMGRDIKVFQSGGNN 72
DB 16 RLIMVGAAGVALLSLGLVGVGGATASAFSPRLPVEYLQVPSMGRNIKVFQSGGAN 75

QY 73 SPAYLLDGLRAODDNGWDINTPAFEWYQSGLSIVMPVGGSSFYSDWYSPACGKAGC 132
DB 76 SPAYLLDGMRAODDNGWDINTPAFEWYQSGISVAMPVGGSSFYSDWYSPACGKAGC 135

QY 133 QTYKWTFTLSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPDQFVYAGLSAL 192
DB 136 TTYKWTFTLSELPAVLASNKQVKPTGSAAGLSMAGSSAMILAAVHPDQFVYAGLSAL 195

QY 193 LDPDSQMGPSLIGLAMGDAGGYKADWGPSPDPAWRNDPTQIQPKLVANNTLWYCG 252
DB 196 LDPDSQMGPSLIGLAMGDAGGYKADWGPSPDPAWRNDPTQIQPKLVANNTLWYCG 254

QY 253 NGTPNELGGANI PAEFLNENFVRSSNLKFQDAYNAAGHNAVFPNPNNGTHSWYWGQALN 312

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Db 255 DGKPSDLGGNNLPKFLGFRVTSNLKFOEAYNGAGGHNVAFFDANGTHDFWYGPVQ 314
 QY 313 AMKGDLOSSLGA 324
 Db 315 AMKGDLOSSLGA 326

RESULT 12
 A85A MYCLE STANDARD; PRT; 330 AA.
 AC Q05861.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-A precursor (85A) (Antigen 85 complex A) (Ag85A) (Mycoly1 transferase 85A) (EC 2.3.1.-) (Fibronectin-binding protein A).
 GN FBPA OR ML0097.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Thai53;
 RX MEDLINE=95130993; PubMed=7829901;
 RA Yin Y.;
 RT "Molecular cloning of alpha antigen like protein gene of Mycobacterium leprae and its over production in Escherichia coli.";
 RL Kansenshogaku Zasshi 68:1330-1337(1994).
 RP [2]
 RP SEQUENCE FROM N.A.
 RA de Mendonca-Lima L.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Hamlin N., Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrall B.G.;
 RA "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 RN [4]
 RP SEQUENCE OF 143-330 FROM N.A.
 RX MEDLINE=93366419; PubMed=8359887;
 RA Rinke de Wit T.F., Bekelie S., Osland A., Wiele B., Janson A.A.M., Thole J.E.R.;
 RT "The Mycobacterium leprae antigen 85 complex gene family: identification of the genes for the 85A, 85C, and related MP751 proteins.";
 RL Infect. Immun. 61:3642-3647(1993).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A MYCOLITRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: CONTAINS ONE DISULFIDE BRIDGE (BY SIMILARITY).
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.

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 CC -----
 CC EMBL; D43841; BAA07864.1; -;
 CC EMBL; M90648; AAA91864.1; -;
 CC EMBL; AL583917; CAC29605.1; -;
 CC EMBL; Z21950; CAA79948.1; -;
 CC DR PIR; A86921; A86921.
 CC DR PIR; S32107; S32107.
 CC DR HSSP; P31953; 1DQY.
 CC DR Leproma; ML0097; -;
 CC DR InterPro; IPR000801; Esterase_put.
 CC DR Pfam; PF00756; Esterase; 1.
 KW Transferase; Acyltransferase; Signal; Antigen; Complete proteome.
 FT SIGNAL 1 42 POTENTIAL.
 FT CHAIN 43 330 ANTIGEN 85-A.
 FT ACT_SITE 168 168 BY SIMILARITY.
 FT ACT_SITE 272 272 BY SIMILARITY.
 FT ACT_SITE 304 304 BY SIMILARITY.
 FT CONFLICT 149 149 Q -> E (IN REF. 1).
 SQ SEQUENCE 330 AA; 35411 MW; 170C7C98C98FC5EC CRC64;
 Query Match 76.7%; Score 1338.5; DB 1; Length 330;
 Best Local Similarity 76.9%; Pred. No. 6.1e-94;
 Matches 240; Conservative 30; Mismatches 41; Indels 1; Gaps 1;
 QY 13 RRLMIGTAAAVLPGILVGLAGGAATAGAFSPGLPVEYLQVPSPMGRDIKVQFQSGNN 72
 Db 16 RRLVVEAMGVALLSALIGV-GSAPAEAFSPGLPVEYLQVPSPMGRDIKVQFQSGAN 74
 QY 73 SPAVYLLDGLRAQDDYNGWDINTPAFWYQSGLSIVMPVQSGSFYSDWYSPAGCKAGC 132
 Db 75 SPALYLLDGLRAQDDYNGWDINTPAFWYQSGLSIVMPVQSGSFYSDWYSPAGCKAGC 134
 QY 133 QTYKWETFLTSFLPQWLSANRAVKPTGSAALGLSMAGSSAMILAAHYHPOQFIYAGSL 192
 Db 135 QTYKWETFLTSFLPQWLSANRAVKPTGSAALGLSMAGSLALTAIYHPDQFIYVGSMSGL 194
 QY 193 LDPSQGMPSLIGLAMGDAGYKAADMWGPSSDPWERNPTQOIPKLVANNTLWYVCG 252
 Db 195 LDPSNMGPSLIGLAMGDAGYKAADMWGPSTDPWERNPTQOIPKLVANNTLWYVCG 254
 QY 253 NGTPNELGGANIPAEFLNFVRSSNLKFDQAYNAAGHNVAFFPPNGTHSWYWGQOLN 312
 Db 255 NGKPTLGGNNLPAKLEGLVRSNPKFDQAYNAGGHNVAFFPPDSGTHSWYWGQOLN 314
 QY 313 AMKGDLOSSLGA 324
 Db 315 DMKPDLOQYLGA 326

RESULT 13
 A85C MYCTU STANDARD; PRT; 340 AA.
 AC F31953; P96806;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mycoly1 transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C).
 GN FBPC OR MP745 OR RV0129C OR MT0137 OR MTC15.03C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Erdmann;
 RX MEDLINE=91348869; PubMed=1715324;
 RA Content J., la Cuvelier A., de Wit L., Vincent-Levy-Frebault V., Ooms J., de Bruyn J.;
 RA "The genes coding for the antigen 85 complexes of Mycobacterium tuberculosis and Mycobacterium bovis BCG are members of a gene

ID AC Q05862; STANDARD; PRT; 333 AA.
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mycoly-
 GN FBPC OR FBPC2 OR ML2655).
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93366419; PubMed=8359887;
 RA Rinke de Wit T.F., Bekelie S., Osland A., Wiele B.,
 RA Janson A.A.M., Thole J.E.R.;
 RT "The Mycobacterium leprae antigen 85 complex gene family:
 RT identification of the genes for the 85A, 85C, and related MPT51
 RL proteins.";
 RL Infect. Immun. 61:3642-3647(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX de Mendonca-Lima L.;
 RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Biglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Rutter L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Squares S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
 CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
 CC MYCOLYTIC TRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
 CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
 CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
 CC N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Z21951; CAA79949.1; -;
 DR EMBL; M90649; AAA91865.1; -;
 DR EMBL; AL583926; CAC32187.1; -;
 DR PIR; S32114; S32114.
 DR HSP; F31953; IDQY.
 DR Leproma; ML2655; -;
 DR InterPro; IPR000801; Esterase; 1.
 DR Pfam; PF00756; Esterase; 1.
 KW Transferase; Acyltransferase; Antigen; Signal; Complete proteome.
 FT SIGNAL
 FT CHAIN 1 46 POTENTIAL.
 FT ACT SITE 47 333 ANTIGEN 85-C.
 FT ACT SITE 170 170 BY SIMILARITY.
 FT ACT SITE 274 274 BY SIMILARITY.
 FT ACT SITE 306 306 BY SIMILARITY.
 SQ SEQUENCE 333 AA; 36392 MW; 50EADF1731E8EC2 CRC64;

Query Match 67.0%; Score 1170; DB 1; Length 333;
 Best Local Similarity 69.3%; Pred. No. 3.1e-81;
 Matches 214; Conservative 33; Mismatches 60; Indels 2; Gaps 1;
 QY 14 RIMTGTAANVPLGLVLAGGAATAGAFSRPLPVEYLQVFPSPSGMRDVKVQFQSGGNN 73
 DB 20 RLTAIVIGTALLAGLVGVGDTAIAVAFSPKPLPVEYLQVFPSPSGMRDVKVQFQSGGQH- 78
 QY 74 PAVYLLDGLRAQDDYNGWDINTPAFEYVYQSLVIMVGVGGSSPYSWYSPACGAGCQ 133
 DB 79 -AVYLLDGLRAQDDYNGWDINTPAFEYVYHSGLSVIMVGVGGSSPYSWYSPQCGQHY 137
 QY 134 TYKWETLTSELPOWLSANRAVKVKTGSAAGLSMAGSSAMILAAVHPQOFLYAGSLSALL 193
 DB 138 TYKWETLTQEMPSLQANKVLTGNAVGLSSGSSALLILASYPOQFFYAAASLSGFL 197
 QY 194 DPSQMGPSLIGLAMGAGGYKAADWMPSSDPAWERNRDTQQIPKLVANNTRLWVYCGN 253
 DB 198 NPSEGWPFTMIGLAMNDSSGYNANSMWGPSTDPARKNDPMVQIPRLVANNTRLWVYCGN 257
 QY 254 GTPNELGGANIPAFELFENFVRSSNLKFDQDAYNAGGNHNAVFPFPPNGTHSWYWGAGQINA 313
 DB 258 GAPNELGGDNIAPKPLESLTLSTNEIFONTYAAAGSGRGNVFNFPFPPNGTHSWYWGAGQINA 317
 QY 314 MKGDLQSSL 322
 DB 318 MKPDIIQIL 326

RESULT 15
 A85C MYCAV STANDARD; PRT; 352 AA.
 ID A85C MYCAV STANDARD; PRT; 352 AA.
 AC O52972;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mycoly-
 DE transferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C).
 GN FBPC.
 OS Mycobacterium avium.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 NCBI_TaxID=1764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15769;
 RX MEDLINE=97427949; PubMed=9284137;
 RA Ohara N., Ohara-Wada N., Kitaura H., Nishiyama T., Matsumoto S.,
 RA Yamada T.;
 RT "Analysis of the genes encoding the antigen 85 complex and MPT51 from
 RT Mycobacterium avium.";
 RL Infect. Immun. 65:3680-3685(1997).
 CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
 CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
 CC MYCOLYTIC TRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
 CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
 CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
 CC N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.
 CC
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 CC
 DR EMBL; D87323; BAA24161.1; -;
 DR HSP; F31953; IDQY.
 DR InterPro; IPR000801; Esterase; 1.
 DR Pfam; PF00756; Esterase; 1.

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KW Transferase; Acyltransferase; Antigen; Signal.
FT SIGNAL 1 46 POTENTIAL.
FT CHAIN 47 352 ANTIGEN 85-C.
FT ACT SITE 170 170 BY SIMILARITY.
FT ACT SITE 274 274 BY SIMILARITY.
FT ACT SITE 306 306 BY SIMILARITY.
SQ SEQUENCE 352 AA; 37756 MW; A29277CB650D60A4 CRC64;

Query Match 66.8%; Score 1165; DB 1; Length 352;
Best Local Similarity 66.4%; Pred. No. 7.9e-81;
Matches 215; Conservative 39; Mismatches 64; Indels 6; Gaps 2;

QY 6 RKIR----AWGRIMIGTAAAVLVPLGLVLAGAAGTAGAFSPRGGLPYEYLQVPSMGRD 61
DB 8 RKLGRGAAATMPRELALAAVUGASLLGVAVAGGSPVAGAFSKPLPYEYLEVPSMGRN 67

QY 62 IKVQFGSGNNFAVILLGLRADDYNGWDINTPAFEWYQSGLSLTVMPVGQSGSFYS 121
DB 68 IKVQFGGGPH--AVILLGLRADDYNGWDINTPAFEWYQSGLSLTVMPVGQSGSFYS 125

QY 122 WSPACGKAGCQTKWETFLTSELPWLSANRAVKPTGSAAGLSMAGSAMILAAVHPQ 181
DB 126 WYFSSNGQNYIKWETFLTSELPWLSANRAVKPTGSAAGLSMAGSAMILAAVHPQ 185

QY 182 QFIYAGLSALLDPSQGMPSLIGLWAGDAGGYKAADMWGPSSDPAPERNDPTQOIPKL 241
DB 186 QFYAASLSGLFNPSEGWWFTLLGLAMNDSGYNANSMWGPSTDPKWRNDPMVQIPRLV 245

QY 242 ANNTLWYCGNTPNELGGANIPAEFLNFRSSNLKFDAYNAAGHNAVFPPNGT 301
DB 246 ANNTLWYCGNTPNELGGANIPAEFLNFRSSNLKFDAYNAAGHNAVFPPNGT 305

QY 302 HSEYWGAGLNAKMGDLOSLGAG 325
DB 306 HSEYWGAGLNAKMGDLOSLGAG 329

RESULT 16
A85A MYCWR STANDARD; PRT; 139 AA.
AC Q9KH57;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 85-A (85A) (Antigen 85 complex A) (A985A) (Mycoly transferase
DE 85A) (EC 2.3.1.-) (Fibronectin-binding protein A) (Fragment).
GN FBPA.
OS Mycobacterium marinum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 2275;
RA Stear T.P., Jenkin G.A., Johnson P.D.R., Davies J.K.;
RT "Comparative genetic analysis of Mycobacterium ulcerans and
RT Mycobacterium marinum reveals evidence of recent divergence.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR
CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A
CC MYCOLYTIC TRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF
CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY
CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: CONTAINS ONE DISULFIDE BRIDGE (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE
CC N-TERMINAL OF C. GLUTAMICUM P51 PROTEIN.
CC

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Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;

"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains";

Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

[4]

SEQUENCE FROM N.A.

SPECIES=M.DOVIS; STRAIN=BCG / Tokyo;

MEDLINE=95242057; PubMed=7725062;

Ohara N., Kitaura H., Hotokezaka H., Nishiyama T., Wada N., Matsumoto S., Matsuo T., Naito M., Yamada T.;

"Characterization of the gene encoding the MP951, one of the major secreted protein antigens of Mycobacterium bovis BCG, and identification of the secreted protein closely related to the fibronectin binding 85 complex.;"

Scand. J. Immunol. 41:433-442(1995).

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE N-TERMINAL OF C.GLUTAMICUM PSI PROTEIN.

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EMBL; AJ002150; CAA05211.1; -

EMBL; AL022076; CAA17867.1; -

EMBL; AL0007185; AAK48276.1; ALT_INIT.

EMBL; D26486; BAA05497.1; -

PIR; G70887; G70887.

HSPP; P31953; IDQ.

TIGR; MT3910; -

TubercuList; RV3803c; -

InterPro; IPR000801; Esterase_put.

Pfam; PF00756; Esterase; 1.

Transferase; Acyltransferase; Signal; Antigen; Complete proteome.

SIGNAL 1 33 POTENTIAL.

CHAIN 34 299 MPT51/MPB51 ANTIGEN.

CONFLICT 246 246 A -> T (IN REF. 1).

SEQUENCE 299 AA; 331089 MW; 4E2E38F87AEDD73E CRC64;

Query Match	29.7%; Score 519; DB 1; Length 299;	38.7%; Pred. No. 3.3e-32;	39; Mismatches 124; Indels 16; Gaps 5;
Best Local Similarity	38.7%;	Pred. No. 3.3e-32;	
Matches 113; Conservative	39;	Mismatches 124; Indels 16; Gaps 5;	
QY 33	GGAAATAGASRRGLPVEYLQVPSDGMGRDIKVFQFSGNNSPAVYLLDGLRAQDDYNGWD	92	
Db 21	GGVVAAREPTAKAAYENLMVSPSGMRDIPVAFLAGGPH--AVLLDAFNAGPDVSNVW	78	
QY 93	INTPAFEWYQSGLSIVMPVGQSSFYSDWSPACGKAGCCTYKWFETLISELPQWLISAN	152	
Db 79	TAGNAMNTLAGKISVAVAPAGATSMYTNWQDG-----SKOWDTFLSAELPDWILAA	131	
QY 153	RAVKPTGSAATGLSWAGSSAMILAAHPQOFIYAGLSLALIDPSQGMGPSLILGLAMGDAG	212	
Db 132	RGLAPGGHAAVGAAGGGYGAMALAAAFHPDRFCFAGSGMGFLYPSNTTNGAIAAGMQOFG	191	
QY 213	GYKAADMWGPSSDPAWERNDDPTQIPLKIVANNITLWYCGNGTNPNELGGANIPAEFLNF	272	
Db 192	GVDITNGWGAQPLGKWKHDDPWVHSLUQAQNTTEVWVW----SPTN--PGASDPAAMIGQA	246	
QY 273	VRS--SNLKFDAYNAAGHNAVENFFPNGTHSWEYWGAIQNAKMGDLQSSL	322	
Db 247	AEAMGNSRMFYNYRVSQGHGHDFDPASGDNGWGSWAPQLGAMSGDIVGAI	298	
RESULT 18			
ID -MPT5 MYCLE			
AC Q05868; Q50207;	STANDARD;	PRT;	301 AA.

	QY	15	LMIQTAAAVVLPGVLAGGAATAGAFSPGLPVEYLQVPSPWGRDILKVFOSGCGNNSP	74
	Dd	16	LAVGVFAAIVL--LAGTAGNAKAAG-----YESLMVESNANGRDIPIVAFWAGGPH--	63
	QY	75	AVYLLDLGLRAQQDDNYNGWDINTPEFWYYQSGLSITMPVGQSSFSYDWYSPACKGACQT	134
	Dd	64	AVYLLDAFNAALDVSNVWTAGNAMTLGGRGISVVAPAGGAYSMTTWENDG-----S	116
	QY	135	YKWETFLSELPSOWLSANRAVKPTGSAAIGLSMAGSSAMILAAYHPPOFTIYAGSLNALID	194
	Dd	117	KQWDTFLSSELPDMLATRKGLPADPDGHAAVGASOGGYAALAALAHFHDPDFGFAGSLSGFY	176
	QY	195	PDSQGMPSLI GLMGDAGGYKAADWGPFSDPAWERNDPTCQIPKLVANNTRLWVYCNG	254
	Dd	177	PSTNYNGAILLAGQQFGDIGNGMWGAQPQLGRWKWHDPYVHASLLAQNNTRVVY----	232
	QY	255	TNELGGGANIPAELDENFVS--SNLKFDQDAYNAAGGNHAVFNPPNGTSHWEVWGAQLIN	312
	Dd	233	SPTWGG-DIDA-MIQAVASMGSSREFYQQYRSVGGNHGHDFSGGDNGAWAPQLA	290
	QY	313	AMKGDLOSSL 322	
	Dd	291	AMS GDIVGAI 300	

RESULT 19
CSPL CORGL

ID	-	CSPL	CORGL	STANDARD;	PRT;	657 AA.
AC		Q0137;				
DT		01-JUL-1993	(Rel. 26, Created)			
DT		28-FEB-2003	(Rel. 41, Last sequence update)			
DT		28-FEB-2003	(Rel. 41, Last annotation update)			
DE		PS1	protein precursor.			
DN		CSPL OR CGL2875.				
OS		Corynebacterium glutamicum (Brevibacterium flavum).				
OC		Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC		Corynebacterineae; Corynebacteriaceae; Corynebacterium.				
NCHI_TaxID=1718;						
RX	[1]	SEQUENCE FROM N.A.				
RC		STRAIN=ATCC 17965 / Melassecola;				
EX		MEDLINE=93023863; PubMed=1406274;				
RA	Jolliff G., Mathieu L., Hahn V., Bayan N., Duchiron F., Renaud M.,					
RA	Sheehar E., Leblon G.;					
RT	"Cloning and nucleotide sequence of the cspl gene encoding PSI, one					
RT	of the two major secreted proteins of Corynebacterium glutamicum: the					
RT	deduced N-terminal region of PSI is similar to the Mycobacterium					
ET	antigen 85 complex.";					
RL	Mol. Microbiol. 6:2349-2362(1992).					
[2]						
RE	SEQUENCE FROM N.A.					
RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;					
RA	Nakagawa S.;					
RL	Submitted genomic sequence of Corynebacterium glutamicum ATCC 13032."					
CC	-!- FUNCTION: ONE OF THE TWO MAJOR SECRETED PROTEINS.					
CC	-!- SUBCELLULAR LOCATION: Secreted.					
CC	-!- SIMILARITY: THE N-TERMINAL IS VERY SIMILAR TO THE COMPLETE					
CC	SEQUENCES OF THE MYCOBACTERIAL ANTIGENS 85-A, 85-B & 85-C.					
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CC	entities requires a license announcement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
DR	EMBL; X66078; CAU46877.1; --					
DR	EMBL; AF005283; HAC00269.1; --					
DR	FIR; S25184; S25184.					
DR	HSP; P31953; IDOZ.					

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complete genome sequence." ;
RL Nature 393:537-544 (1998) .
RN [2]
RC SEQUENCE FROM N.A.
RP STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains." ;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- DOMAIN: LYSM REPEATS ARE THOUGHT TO BE INVOLVED IN PEPTIDOGLYCAN
CC BINDING.
CC -1- SIMILARITY: SOME, TO MYCOBACTERIUM A85 ANTIGENS.
CC -1- SIMILARITY: Contains 3 LysM repeats.
CC -----
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CC -----
DR EMBL; Z734119; CAA97754.1; .-
DR EMBL; AE007007; AAK45587.1; .-
DR PIR; D70772; D70772.
DR TIGR; MT1326; .-
DR Tuberculist; RV1288; .-
DR InterPro; IPR000801; Esterase_put.
DR InterPro; IPR002482; LysM.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00756; Esterase; 1.
DR Pfam; PF01476; LysM; 3.
DR SMART; SM00257; LysM; 3.
DR KW Hypothetical protein; Repeat; Complete proteome.
FT REPEAT 5 51 LYSM 1.
FT REPEAT 56 102 LYSM 2.
FT REPEAT 107 153 LYSM 3.
FT REPEAT
SQ SEQUENCE 456 AA; 49618 MW; 9B70C0471EDF113A CRC64;
Query Match 8.4%; Score 146.5; DB 1; Length 456;
Best Local Similarity 25.7%; Pred. No. 0.00066;
Matches 68; Conservative 34; Mismatches 86; Indels 77; Gaps 16;
QY 66 FQSGGNNSPAVYLLDGLRAQDDYNGWDI-----NTPAFEWYYQSGLSIIVPVGGOSS 117
Db 198 YRTSGRTYVLYLFGGGTDQFRTEFLGIRDLTAGRP-----IIIVPDGGHAG 248
QY 118 FYSDDWYSPACGKAGCTYKWTFLTSELPLQWLSAN--RAVKPTGSAALGSLWAGSSAMIL 175
Db 249 WYGNPVSSVFGPR-----NWETFHTIAQLLPWTEANFRTVAEYDGRAVAGFSMGFGALKY 303
QY 176 AAYHPQOQFYAGLSALLDPSQMGPSLI-----GL-----AMGDAGYKAAADWMGP 222
Db 304 AAKYGHFASASHS-----GPASLRDRDFGLVHWEHANLSSAVLDLGG---GTVYGA 351
QY 223 SSDPAPER-----NDPTQOIPKLVANTRLWYCGNG-----TENE--LGCNIPA 266
Db 352 ---PLWDQARVSADNPVERIDSY--RNKRFILVAGTSPDPANWFDVNETQVLAGQR--- 403
QY 267 EPLENFVRSNLFK-QDAYNAAGGH 290
Db 404 EPRE---RLSNAGIPHESHEVGGH 425
RESULT 21
ESTD HUMAN
ID ESTD_HUMAN STANDARD; PRT; 282 AA.
AC F10768;
NC 01-JUL-1989 (Rel. 11. Created)

```

01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Esterase D (EC 3.1.1.1).
ESD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=88272298; PubMed=3164702;
RX Young L.-J.S., Lee E.Y.-H.P., To H., Shields R., Shew J.-Y.,
RA Donoso L.A., Sery T., Giblin M., Fields J.A., Lee W.-H.;
RA "Human esterase D gene: complete cDNA sequence, genomic structure,
RT and application in the genetic diagnosis of human retinoblastoma";
RL Hum. Genet. 79:137-141(1988).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Hypothalamus;
RX MEDLINE=20402571; PubMed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RN axis and full-length cDNA cloning";
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
[3]
RN PRELIMINARY SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=86313576; PubMed=3462698;
RA Lee E.Y.-H.P., Lee W.-H.;
RT "Molecular cloning of the human esterase D gene, a genetic marker of
RN retinoblastoma";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6337-6341(1986).
[4]
RN SEQUENCE OF 150-186 FROM N.A., AND SEQUENCE OF 150-175.
RX MEDLINE=86313620; PubMed=3462714;
RA Squire J., Dryja T.P., Dunn J., Goddard A., Hofmann T.,
RA Musarella M., Willard H.F., Becker A.J., Gallie B.L., Phillips R.A.;
RT "Cloning of the esterase D gene: a polymorphic gene probe closely
RN linked to the retinoblastoma locus on chromosome 13";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6573-6577(1986).
[5]
RN SEQUENCE OF 168-200 FROM N.A.
RA Tsuchida S., Ikemoto S., Kajii E.;
RN Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN VARIANT GLU-190.
RX MEDLINE=94171223; PubMed=7907313;
RA Tsuchida S., Fukui E., Ikemoto S.;
RT "Molecular analysis of esterase D polymorphism";
RN Hum. Genet. 93:255-258(1994).
CC -|- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -|- SUBUNIT: Homodimer.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC VESICLES.
CC -|- POLYMORPHISM: THERE ARE TWO MAJOR ELECTROPHORETIC ISOTYPES. THE
CC SEQUENCE OF THE ESD 1 VARIANT IS SHOWN.
CC -|- SIMILARITY: STRONG, TO YEAST HRE299.
CC -|- SIMILARITY: VERY LOW, TO TYPE-B CARBOXYLESTERASES.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M13450; AAA52408.1; ALT SEQ.
DR EMBL; AF112219; AAC99788.1; -
DR EMBL; AF052509; AAC06298.1; -

FOR ALPHA-GLUCOSIDES SUCH AS SUCROSE, MALTOSE AND TREHALOSE.
 CC SUBCELLULAR LOCATION: Periplasmic (Probable)
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 CC PROTEIN FAMILY 1.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AF045609; AAD12050.1; ALT_INIT.
 CC EMBL; AL591784; CAC45267.1; -
 CC InterPro: IPR006061; SBP_dom1.
 CC Pfam; PF01547; SBP_bac_1; 1.
 CC PROSITE; PS01037; SBP_BACTERIAL_1; FALSE NEG.
 CC Sugar transport; Transport; Periplasmic; Signal; Complete proteome.
 KW SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 458 ALPHA-GLUCOSIDES-BINDING PERIPLASMIC
 FT PROTEIN AGLE.
 SQ SEQUENCE 458 AA; 49703 MW; E7A7F8157C2FC291 CRC64;
 Query Match 6.6%; Score 116; DB 1; Length 458;
 Best Local Similarity 23.1%; Pred. No. 0.13;
 Matches 83; Conservative 27; Mismatches 118; Indels 132; Gaps 17;
 QY 13 RLRLMTGTAAYVPLGLVGLAGGATAGAFSRPG-----LPVEYLQVP 54
 DB 3 RSLLTGVAFAALLAGTAGLAGTAGAADLKFKFGEDSRFNWASLEEFKKGHDLKGQTLTIF 62
 QY 55 SPSMGDR-----IKVQFSGGNNSPAVYLLDGLRAQDYNGDINTPAF 98
 DB 63 GPWRGEDEALFKSVYVFEATGVELKYSSENVEQIV-----DTQAG---SPDV 112
 QY 99 EMYQSGL-----SIVMPVGGQSFYSDWSPACGKAGCQTYKWTETLTSELPOWLSA 151
 DB 113 AILPQPLGIADLAARGLLTPLG-----DETQWLID 143
 QY 152 NEAVKPTGSAATGLS-----MAGSSAMI-----LAAYHPOQFIYAG-----SL 189
 DB 144 NYA---AGQSWDLSTYNGKDTGTSALYAFYKIDVKSIVYVPEFEDAGYEYKTEEL 200
 QY 190 SALLD--PSQGMGPSLIGLMDAGGYKAADMWGPSSDPFAWRNDTQOIPKLIVANTRL 247
 DB 201 KALTEKIAEDGKPCWICIGLGGCATGWPTD-W---VEDIMLTQPAFTYDKWKVKNRIFP 256
 QY 248 WYVCGMTGNELGGANIPAEFLNFVRSNNLKFQDAVNAAGGHNAV----FNPPPGNTHS 303
 DB 257 TDAAVTGALEFGW-----FARN-----DAF-VDGGAANAVSTDRSPKGLFS 299
 RESULT 23
 XAMP_XANS2 STANDARD; PRT; 827 AA.
 AC Q60106;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Xanthomonas pepsin precursor (EC 3.4.21.101) (Xanthomonas aspartic
 DE proteinase) (Carboxyl proteinase) (XCP).
 OS Xanthomonas sp. (strain T-22).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 NCBI_TaxID=136420;
 [1]
 SEQUENCE FROM N.A., AND CHARACTERIZATION.
 MEDLINE=97058302; PubMed=8902622;
 Oda K., Ito M., Uchida K., Shibano Y., Pukuhara K.-I., Takahashi S.;
 "Cloning and expression of an isovaleryl peptstatin-insensitive
 carboxyl proteinase gene from Xanthomonas sp. T-22.";
 J. Biochem. 120:564-572(1996).

DR PIR; A23543; A23543.
 DR Genew; HGNC:3465; ESD.
 DR MIM; 133280; -
 DR GO; GO:0016023; C:cytoplasmic vesicle; NAS.
 DR GO; GO:0004759; F:serine esterase activity; NAS.
 DR InterPro; IPR000801; Esterase_put.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR Pfam; PF00756; Esterase; 1.
 KW Hydrolase; Serine esterase; Polymorphism.
 FT ACT SITE 149 149 POTENTIAL.
 FT VARIANT 190 190 G -> E (IN ESD 2; dbSNP:1051064).
 FT /FTID=VAR_005202.
 SQ SEQUENCE 282 AA; 31463 MW; BFC20D5FA2B9DCE CRC64;
 Query Match 7.2%; Score 125; DB 1; Length 282;
 Best Local Similarity 21.2%; Pred. No. 0.016;
 Matches 52; Conservative 38; Mismatches 91; Indels 64; Gaps 9;
 QY 74 PAVYLLDGLRAQDYNGDINTPAFWEYQS-----GLSIVMP-----V 112
 DB 46 PALYWLGLTCTEQ-----NFIKSGYHQSAEHLVVIAPDTPRCNKGEDSWDF 99
 QY 113 GQSGSFYSD-----WYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKTGSAIGLUM 167
 DB 100 GTGAGFYVDATEDPKT-----NYPMYSYVTEELPOLINANFPVDPQRMSTFGHSM 150
 QY 168 AGSSAMILAAVHPQOQFIYAGLSALLDPSQGMGPSLIGLMDAGGYKAADMWGPSSDPA 227
 DB 151 GGHGALICALKNPGKYSVAFAPICNPV-----LCP-----WGKFAFGYLGTDSK 198
 QY 228 WERNPTQOIPKLIVANTRLWYVCGNTPNELGGANIPAEFLNFVRSN-----LKF 280
 DB 199 WKAYDATHLVKSPGSQLDILIDQGDQDQFLDGLLP-----DNFIACTEKKIPVVFRL 254
 QY 281 QDAYN 285
 DB 255 QEGYD 259
 RESULT 22
 AGLE_RHIME STANDARD; PRT; 458 AA.
 AC Q9Z3R5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE alpha-glucosides-binding periplasmic protein agle precursor.
 GN AGLE OR R00695 OR SMC03061.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 NCBI_TaxID=382;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=99328961; PubMed=10400573;
 Willis L.B., Walker G.C.;
 RA "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase
 and a periplasmic-binding-protein-dependent transport system for
 alpha-glucosides.";
 RL J. Bacteriol. 181:4176-4184(1999).
 [2]
 SEQUENCE FROM N.A.
 STRAIN=1021;
 MEDLINE=21396507; PubMed=11481430;
 Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetalle D., Puehler A., Purnelle B., Ramsperger U.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
 RA "Analysis of the chromosome sequence of the legume symbiont
 Sinorhizobium meliloti strain 1021.";
 Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

RN [2]
 RP MUTAGENESIS OF ASPARTIC ACID AND GLUTAMIC ACID RESIDUES, AND ACTIVE
 RX SITES.
 RA MEDLINE=99419069; PubMed=10488127;
 RY Oyama H., Abe S.-I., Ushiyama S., Takahashi S., Oda K.;
 RT "Identification of catalytic residues of pepstatin-inhibitive
 RL carboxyl proteinases from prokaryotes by site-directed mutagenesis.";
 RJ J. Biol. Chem. 274:27815-27822(1999).
 CC -!- CATALYTIC ACTIVITY: Cleavage of casein.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: AUTOCATALYTICALLY PROCESSED.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.
 CC -!- SIMILARITY: CONTAINS 1 PKD DOMAIN.
 CC
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 CC
 CC EMBL; D83740; BAA12093.1; -
 CC MEROPS; S53.002; -
 CC InterPro; IPR000601; PKD domain.
 CC Pfam; PF00082; Peptidase_S8; 1.
 CC Pfam; PF00801; PKD; 1.
 CC Pfam; PF04151; PPC; 1.
 CC SMART; SM00089; PKD; 1.
 CC PROSITE; PS00093; PKD; 1.
 CC Hydrolase; Protease; Serine protease; Zymogen; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 237
 FT CHAIN 238 635
 FT PROPEP 636 827
 FT DOMAIN 635 722
 FT ACT_SITE 406 406
 FT ACT_SITE 544 544
 FT ACT_SITE 585 585
 FT ACT_SITE 585 585
 SQ SEQUENCE 827 AA; 83706 MW; 21A33C4C683DBC8F CRC64;

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 or send an email to license@isb-sib.ch).
 EMBL; Z22595; CAA80310.1; -
 PIR; S39530; S39530.
 InterPro; IPR000379; Ser esters site.
 Hydrolase; Lipid degradation; Signal; Multigene family.
 FT SIGNAL 1 37
 FT CHAIN 38 414
 FT ACT_SITE 154 154
 FT DOMAIN 329 332
 FT DOMAIN 333 338
 FT DOMAIN 343 346
 FT DOMAIN 349 356
 SQ SEQUENCE 414 AA; 43496 MW; C1F7C0CFC59FB111 CRC64;

Query Match 6.1%; Score 106; DB 1; Length 414;
 Best Local Similarity 24.2%; Pred. No. 0.67;
 Matches 60; Conservative 26; Mismatches 96; Indels 66; Gaps 13;
 QY 72 NSPAVLLDG---LRAQDDYNGMDI--NTPAFEWYQSGLSIWPVVGSSFSYSDWSPA 126
 Db 64 NAPLVVALLHGCTQTAAAYEASGWSALGNTHKFFVYVYPQQS-----GNNSKCFNWFEDG 118
 QY 127 CGKAGCQTYKWTFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPQOFIYA 186
 Db 119 DITRG---QGEALSIKQWDMNKNANHSIDPSRVYVTGLSAGAFMTVMAATVPDVFAGA 174
 QY 187 GSLG-----ALLDPSQMGPSLLIG-LAMGAGGYKA-----ADWWGPPSSD-- 225
 Db 175 APIAGGPYKCATSMTSFAFTCMSPGVKTPAAGMDLARGYSGYNGPKKISIHGSSDYT 234
 QY 226 ---PAWERNDPTQO-----IPKLIV---ANNTRL-----WYCCNGNTP 256
 Db 235 VAPA-NQNETVEQFTNYHGIDQTPDVSDTVGFGFHKVKSANGTPLVETTYITGMGHGTP 293
 QY 257 NELG-GAN 263
 Db 294 VDPGTGAN 301

Query Match 6.1%; Score 106; DB 1; Length 414;
 Best Local Similarity 24.2%; Pred. No. 0.67;
 Matches 60; Conservative 26; Mismatches 96; Indels 66; Gaps 13;

QY 72 NSPAVLLDG---LRAQDDYNGMDI--NTPAFEWYQSGLSIWPVVGSSFSYSDWSPA 126
 Db 64 NAPLVVALLHGCTQTAAAYEASGWSALGNTHKFFVYVYPQQS-----GNNSKCFNWFEDG 118
 QY 127 CGKAGCQTYKWTFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAVHPQOFIYA 186
 Db 119 DITRG---QGEALSIKQWDMNKNANHSIDPSRVYVTGLSAGAFMTVMAATVPDVFAGA 174
 QY 187 GSLG-----ALLDPSQMGPSLLIG-LAMGAGGYKA-----ADWWGPPSSD-- 225
 Db 175 APIAGGPYKCATSMTSFAFTCMSPGVKTPAAGMDLARGYSGYNGPKKISIHGSSDYT 234
 QY 226 ---PAWERNDPTQO-----IPKLIV---ANNTRL-----WYCCNGNTP 256
 Db 235 VAPA-NQNETVEQFTNYHGIDQTPDVSDTVGFGFHKVKSANGTPLVETTYITGMGHGTP 293
 QY 257 NELG-GAN 263
 Db 294 VDPGTGAN 301

RESULT 25
 ID GLIL HUMAN STANDARD; PRT; 1106 AA.
 AC P08151; Q8TDN9;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)

RN [2]
 RP MUTAGENESIS OF ASPARTIC ACID AND GLUTAMIC ACID RESIDUES, AND ACTIVE
 RX SITES.
 RA MEDLINE=99419069; PubMed=10488127;
 RY Oyama H., Abe S.-I., Ushiyama S., Takahashi S., Oda K.;
 RT "Identification of catalytic residues of pepstatin-inhibitive
 RL carboxyl proteinases from prokaryotes by site-directed mutagenesis.";
 RJ J. Biol. Chem. 274:27815-27822(1999).
 CC -!- CATALYTIC ACTIVITY: Cleavage of casein.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: AUTOCATALYTICALLY PROCESSED.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S53.
 CC -!- SIMILARITY: CONTAINS 1 PKD DOMAIN.
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 CC
 CC EMBL; D83740; BAA12093.1; -
 CC MEROPS; S53.002; -
 CC InterPro; IPR000601; PKD domain.
 CC Pfam; PF00082; Peptidase_S8; 1.
 CC Pfam; PF00801; PKD; 1.
 CC Pfam; PF04151; PPC; 1.
 CC SMART; SM00089; PKD; 1.
 CC PROSITE; PS00093; PKD; 1.
 CC Hydrolase; Protease; Serine protease; Zymogen; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 237
 FT CHAIN 238 635
 FT PROPEP 636 827
 FT DOMAIN 635 722
 FT ACT_SITE 406 406
 FT ACT_SITE 544 544
 FT ACT_SITE 585 585
 FT ACT_SITE 585 585
 SQ SEQUENCE 827 AA; 83706 MW; 21A33C4C683DBC8F CRC64;

Query Match 6.2%; Score 109; DB 1; Length 827;
 Best Local Similarity 22.1%; Pred. No. 0.87;
 Matches 63; Conservative 46; Mismatches 114; Indels 62; Gaps 13;
 QY 28 LVGLAGGA-----ATAGASRPLGPEYLVQVPSMGRDIKVFQSGNNSPA 75
 Db 320 IVGIAGGVQLIFPYSANGSSSGITDAGITASYNRAVTDNIKLVN---SLGEDETA 376
 QY 76 VYLLDGLRAQDDYNGMDINTPAFEWYQSGLSIWPVVGSSFSYSDWSPACGACQTY 135
 Db 377 AQ-QSGTQAADDA-----IPQAVA-----QSGT-----FSTAGDAG--VY 410
 QY 136 KNETFTLSLPQWLSANRA-----VKPTGSAAGLSMAGSSAMILAAVHPQOFI 184
 Db 411 QWSTDPSTGSPGV-ANSAGTKIDLTHYSVSEPPSPYIVQGGTILSTSGTTWGGTV 469
 QY 185 YAGLSALADPQCGMPSLIGLWAGDAGGYKAADWMPGSSDPPOWERNDPTQIPKLIVANN 244
 Db 470 WNEGLSIA-PQGGNNQRLWATGGGVSLYEAPSWQSSVSSSTRKVRGPDALFADRASSG 528
 QY 245 TRLWYCYGNGTPELGGANIPAE-PLNFVRSNLFQDAYNAG 288
 Db 529 ALIVV---NGSTEQVGGTSLASPLFVGAFATIESA-----ANNAIG 566

RESULT 24
 ID PHAL PSELE STANDARD; PRT; 414 AA.
 AC P52090;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

Db 620 WRSRAEYPGVNPVAGVTRRASDPQAQADRPAPARVQRFKSLGCVHTPTTVAGGGQNF--D 677

QY 122 WXPACGKAGCQTYKWTETLTSELPQWLSANRAVKPTG---SAAIGLSWAGSAMLAAY 178

Db 678 PVLFP-----TSVYSPQPPSITENAAWDARGLQEEPEVGTSMVGSLNPFYDMF 724

QY 179 HQQFTI-YAGSLUSALLDPQSGMPSLIGLWAGDAGGYKAADWVGSSDDAW-ERNPTQ 236

Db 725 PPTDILGYGPGGAAPYARGPGLGPGPTNY-----GNPCQQQASYPDPTQE 778

QY 237 IPLKVVNTRLW-----VTCNGTNPNELGANIPAEFLNF 272

Db 779 -----TWGEPFPHSLGYPG---PKALGGTYSQCPLREHY 809

RESULT 26

TOB2 HUMAN

ID TOB2 HUMAN STANDARD; PRT; 344 AA.

AC Q14106; Q9BY97; Q9UBI0;

DT 01-NOV-1997 (Rel. 35, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE TOB2 protein (Transducer of erbB-2 2).

GN TOB2 OR TOB4 (OR KIAAL663).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20071127; PubMed=10602502;

RA Ikematsu N., Yoshida Y., Kawamura-Tsuzuku J., Ohsugi M., Onda M.,

RA Hirai M., Fujimoto J., Yamamoto T.;

RT "Tob2, a novel anti-proliferative Tob/BTG1 family member, associates

RT with a component of the CCR4 transcriptional regulatory complex

RT capable of binding cyclin-dependent kinases.";

RL Oncogene 18:7432-7441(1999).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=211156230; PubMed=11258795;

RA Hirose M., Nagase T., Muranashi Y., Kikuno R., Ohara O.;

RT "Identification of novel transcribed sequences on human chromosome 22

RT by expressed sequence tag mapping.";

RL DNA Res. 8:1-9(2001).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20057165; PubMed=10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,

RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,

RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,

RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.B., Cole C.G., Collier R.E., Connor R.,

RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Evans K.L., Fey J.M., Fleming K., French L.M., Ellington A.G.,

RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tanley G., Heathcote R.W., Ho S., Holmes S.,

RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,

RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,

RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,

RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,

RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,

RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,

RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,

RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,

RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,

RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,

RA Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L.,

RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,

RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,

RA Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P.,

RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,

RA Tilahun Y., Wright H.;

RT "The DNA sequence of human chromosome 22.";

RT Nature 402:489-495(1999).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C.,

RA Bosak S.A., McRwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Anti-proliferative protein inhibits cell cycle

CC progression from the G0/G1 to S phases.

CC -!- SUBUNIT: Associates with CAP1.

CC -!- TISSUE SPECIFICITY: Ubiquitous.

CC -!- SIMILARITY: BELONGS TO THE BTG FAMILY.

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CC EMBL; D64109; BAA10971.1;

DR EMBL; AB035207; BAA87042.1;

DR EMBL; AB051450; BAA33333.1; ALT_INIT.

DR EMBL; AL008582; CAB62938.1;

DR EMBL; BC038957; AAH38957.1;

DR MIM; 607396;

DR GO; GO:0005634; Cnucleus; TAS.

DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.

DR GO; GO:0007292; P:ogenesis; TAS.

DR GO; GO:0000074; P:regulation of cell cycle; TAS.

DR InterPro; IPR002087; Anti_prolifcn.

DR Pfam; PF01211; Anti_proliferat; 1.

DR PRINTS; PR00310; ANTIPRLFTG1.

DR SMART; SM00099; btg1; 1.

DR PROSITE; PS00960; BTG_1; 1.

DR PROSITE; PS01203; BTG_2; 1.

FT CONFLICT 34 35 RL -> QA (IN REF. 1; BAA10971).
FT CONFLICT 214 214 P -> H (IN REF. 1; BAA10971).
FT CONFLICT 278 317 QSGTGPFGSGAGTGNSSFDMAQVFGGANSLELEKT
FT FT -> RAAAPQARLEAVGLAPATAAALTWPRYLEVVPPTASSWR
FT FT RH (IN REF. 1; BAA10971).
FT SEQUENCE 344 AA; 36632 MW; ACE4CD8939641BD5 CRC64;
Query Match 5.8%; Score 101; DB 1; Length 344;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 67; Conservative 41; Mismatches 115; Indels 52; Gaps 12;
QY 40 AFSPGLPVEYLQVPSR---SMGFD-LKQVQSGGNSPAVYLLDGLRLAODYNGWDINT 95
Db 71 AAKESGLAVEDVRANVFEESVWIDPEVSVQIGKGAVKVLYL-----DDSEG--CGA 122
QY 96 PAFEWYQSGLS-----IWPVGGQSSFYSDWYSPACGKAGCQTY-----KWETFLTSLP 146
Db 123 PELDKELSSPNPAQVFPVIGSQDSSLNSPFSFGSPSPTEIPRSAQPIITTTASFA 182
QY 147 QWLSANRAVKPTGSAAGLSWAGSAMLAAHYHQFYAGSLYAGSLALDPSQGMGFSLLGL 206
Db 183 ATKEGSTKMGKGAAGGAVSSGAG--GQPPQPPPMARSPTNSLLKHKSLSLSMHSL 240
QY 207 AMGDAGGYKAADMWCPSSDPAWERNPTQOIPKLVANTRLWYCGNGTEN-----ELG 260
Db 241 NF-----ITANPA-----POSQ-----SPNAKEFVYNGGSPSLFFDAADGQ 278
QY 261 GANIPAELENFVRSSN-LKFQDAYNAAGHNAVF 294
Db 279 GSGTGPFGSGAGTCNSSFDMAQVFGGANSLE 313
RESULT 27
Y967 CORGL STANDARD; PRT; 426 AA.
ID Y967 CORGL
AC P35866;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein Cg10967 (ORF2).
GN CGL0967.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RX MEDLINE=92236417; PubMed=1667221;
RA Seep-Feidhaus A.H., Kalinowski J., Puehler A.;
RT "Molecular analysis of the Corynebacterium glutamicum lys1 gene
involved in lysine uptake."
RL Mol. Microbiol. 5:2995-3005(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; X60312; CAA42856.1; -
CC EMBL; AP005277; BAB98360.1; -
CC PIR; S28812; S28812.
DR InterPro; IPR000801; Esterase_put.
DR InterPro; IPR000379; Ser_estr5_site.

DR Pfam; PF00756; Esterase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 426 AA; 45730 MW; F0482C5F681200D8 CRC64;
Query Match 5.8%; Score 100.5; DB 1; Length 426;
Best Local Similarity 21.5%; Pred. No. 1.8;
Matches 69; Conservative 43; Mismatches 122; Indels 87; Gaps 16;
QY 29 VLAGGA--ATAGAFSRPG---LPVEYLQVPSMGRDIKQVQSGGNSPAVYLLDGLR 83
Db 162 VPLAGTDDTSFGDARDAYAYIPPAWDPNLSQL-----PVLVMPGNP 206
QY 84 AODYNGW-----DINTPAFEWYQSGLSIWMPVGGQSSFYSDWYSPACGKAGCQTYKW 137
Db 207 GQPDQ--WFSNGADQTNFQATHDGIPIVIVSDVTGTSFG--NPACVDSQAQVM- 260
QY 138 EFTLTSLPQWLSAN-RAVXPTGSAAI-GLSMAGSSAMILAAHYHQF-----IYAGSLSA 191
Db 261 -TYLSDHVPMLIKQFRVNDQRTWTIGLSYGTCTALQIWNHPEAYGSLDFSGQEEP 319
QY 192 LLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNPTQOIPKLVANTRLWYVC 251
Db 320 TLGTRQQTVDLFG--GDEDAFKAV-----NPEDLLNQAIS- 354
QY 252 GNGTPELGGANIPAELENFVRSSN-----LKFQDAYNAAGHNAVFPPNGTHSW 304
Db 355 -----GAITYSGISGRFIAGSNKSAVSALSHLDNLSNQAGMSTTFDTVAGG-HSF 404
QY 305 EYWGAQLN-----AMKGLQ 319
Db 405 QWRVALANTFDWVAKRGGLQ 425
RESULT 28
CBPE CANFA STANDARD; PRT; 416 AA.
ID CBPE CANFA
AC P55261;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Carboxypeptidase B precursor (EC 3.4.17.2) (47 kDa zymogen granule
membrane associated protein) (ZAP47).
GN CPB1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Fukuoka S.-I.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: Peptidyl-L-lysine(or L-arginine) + H(2)O =
CC peptide + L-lysine(or L-arginine).
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M14.
CC -----
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CC -----
CC EMBL; D78348; BAA11366.1; -
CC ESSP; P09955; IPHA.
DR MEROPS; M14.003; -
DR InterPro; IPR003146; Propap M14.
DR InterPro; IPR000834; Zn_carbOpept.
DR Pfam; PF02244; Propap M14; 1.
DR Pfam; PF00246; Zn_carbOpept; 1.
DR PRINTS; SM00765; CRHOXYPTASEA.
DR SMART; SM00631; Zn_pept; 1.

DR PROSITE; PS00132; CARBOXYPEPT ZN 1; 1.
 DR PROSITE; PS00133; CARBOXYPEPT ZN 2; 1.
 KW Hydrolase; Carboxypeptidase; Metalloprotease; Zinc; Zymogen; Signal.
 FT SIGNAL 1 15 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT PROPEP 16 109 CARBOXYPEPTIDASE B.
 FT CHAIN 110 416 ZINC (BY SIMILARITY).
 FT METAL 175 178 ZINC (BY SIMILARITY).
 FT METAL 178 178 ZINC (BY SIMILARITY).
 FT METAL 303 303 ZINC (BY SIMILARITY).
 FT ACT_SITE 377 377 NUCLEOPHILE (BY SIMILARITY).
 FT DISULFID 244 267 BY SIMILARITY.
 FT DISULFID 258 272 BY SIMILARITY.
 SQ SEQUENCE 416 AA; 47595 MW; DFE1992CD52F8AB4 CRC64;

Query Match 5.7%; Score 100; DB 1; Length 416;
 Best Local Similarity 21.3%; Pred. No. 1.9;
 Matches 57; Conservative 34; Mismatches 77; Indels 100; Gaps 15;

QY 59 GRDI-KVQFQSGNNSPAVYLLDGLRAQDDYNGWDINTPAF-EWYQSGLSIYMPVGGQS 116
 DB 150 GRTIYLLKVGKAGQKPAIFMDCGFHARE---W--ISPAFWQFVREXIRTY---QGE 199
 QY 117 SFYS-----DWSPACGKAGCQTYKWFELTSELPOWLSANRAVKPTGSAAGLSMAGS 170
 DB 200 IHWTELLDKLDFVLPVGNIDGVYTW-----TKRMWRKTRSTGVGNCVGT 247
 QY 171 SAMILAAYHPQOFIYAGSLALLDPSQGMPSLIGLAMDGAGYKAADMWGPSSDPAPWR 230
 DB 248 -----DTRNF-----DAGWCKI-----GASRNPCDE- 269
 QY 231 NDPTQOIKPLVANTRFLWYCGNGTPNELGGANIPAEFLNFVRSSNLKFDQAYNAAGH 290
 DB 270 -----TYCGPAASEK-----ETKALANFIR-SNLSIKAYLTIHSY 305
 QY 291 NAVENFPNGTHSWEYW-----GAQLNAM 314
 DB 306 SQMMLP-----YSYDYKLTENNAELNAL 329

RESULT 29

WETA EMENI
 ID WETA EMENI STANDARD; PRT; 555 AA.
 AC P22022;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Regulatory protein WETA.
 GN WETA.
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiaceae; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RX MEDLINE=91094871; PubMed=1986246;
 RA Marshall M.A.; Timberlake W.E.;
 RT "Aspergillus nidulans weta activates spore-specific gene expression.";
 RL Mol. Cell. Biol. 11:55-62(1991).
 CC -!- FUNCTION: RESPONSIBLE FOR ACTIVATING A SET OF GENES WHOSE PRODUCTS
 CC MAKE UP THE FINAL TWO CONIDIAL WALL LAYERS OR DIRECT THEIR
 CC ASSEMBLY AND THOUGH THIS ACTIVITY IS RESPONSIBLE FOR ACQUISITION
 CC OF SPORE DORMANCY.
 CC -!- FUNCTION: BRLA, ABAA & WETA ARE PIVOTAL REGULATORS OF CONIDIOPHORE
 CC DEVELOPMENT AND CONIDIUM MATURATION. THEY ACT INDIVIDUALLY AND
 CC TOGETHER TO REGULATE THEIR OWN EXPRESSION AND THAT OF NUMEROUS
 CC OTHER SPORULATION-SPECIFIC GENES.
 CC -!- DEVELOPMENTAL STAGE: THE WETA GENE IS ACTIVATED ONLY DURING
 CC CONIDIOPHORE DEVELOPMENT, AND ITS MRNA ACCUMULATES PREFERENTIALLY
 CC IN MATURE CONIDIA.
 CC -!- DOMAIN: HAS AN ACIDIC N-TERMINUS (AA 1-52) FOLLOWED BY A SER-,
 CC THR-, PRO-RICH DOMAIN (AA 125-233) AND A BASIC C-TERMINUS (AA
 CC 461-555).
 CC -!- SIMILARITY: TO P.CHRYSOGENUM WETA.

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Fri Feb 6 13:54:48 2004

Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RL [4]
 RN IDENTIFICATION.
 RP Rudd K.E.;
 RA Unpublished observations (MAR-1996).
 RL -!- SIMILARITY: STRONG, TO E.COLI YEIG AND H.INFLUENZAE HI0184.
 CC -!- SIMILARITY: STRONG, TO HUMAN ESTERASE D.
 CC -!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 137.
 CC -----
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 CC -----

EMBL; D85613; ; NOT ANNOTATED_CDS.
 DR EMBL; AE000142; AAC73458.1; -;
 DR EMBL; U73857; AAL18080.1; -;
 DR PIR; C64763; C64763.
 DR EcoGene; EG13295; Yalm.
 DR InterPro; IPR00801; Esterase_put.
 DR InterPro; IPR00379; Ser_estr_site.
 DR Pfam; PF00756; Esterase; 1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 277 AA; 31424 MW; C69C708293FA0AEC CRC64;

Query Match 5.6%; Score 97.5; DB 1; Length 277;
 Best Local Similarity 18.8%; Pred. No. 1.9;
 Matches 52; Conservative 42; Mismatches 101; Indels 81; Gaps 11;
 QY 74 PAVYLDGLRAQDDYNGWDINTPAPEWYQSGLS-----IVMP----- 111
 Db 44 PVLYWLSGLTNEQ-----NFITKSGQRYAAEHNIIVVAPDTSRGRSHVADAD 92
 QY 112 ---VGQSSGF-----SDWYSPACGKAGCQTYKWTFTLSELPQWL-----SANRAVKP 157
 Db 93 RYDLGGAGFYLNATQAPWN-----EHYKMYDYIRNELPDLVWHHFPATAKSIS- 142
 QY 158 TGSAAIIGLSNAGSSAMILAAHYHQQFIYAGSLSALLDPSQGMGFSLLGLAMGDAGGYKAA 217
 Db 143 -----GHSNGGLGALVLAIRNPEYVSFAFSPIVSPSQ-----VPWGOQAF 184
 QY 218 DMWGPSSDPARERNDPTQIPKLVANNTRL-WVYCGNGTPELGGANIPAEFTLENFVRSS 276
 Db 185 AAYLAENKDALDYDPV-----SLISQQRVARIWVDGLSDDFYAEQLRTPNLEKICQEM 240
 QY 277 NLKXFDAYNAAGGHNAVFNFPPNGTHSWYWGQQLN 312
 Db 241 NIKTLIRYHGYDHSYFYVSSFIGEHI-AYHANKLN 275

Search completed: February 5, 2004, 17:38:51
 Job time : 18.4762 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:34:22 ; Search time 47.2024 Seconds
(without alignments)
1776.756 Million cell updates/sec

Title: US-09-805-427A-2
Perfect score: 1745
Sequence: 1 MTDVSRKIRAWRRRLMIGTA.....YWGALNAMKGDLSLGLGAG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830521

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SPTREMBL 23:*

- 1: sp archaea:*
- 2: sp bacteria:*
- 3: sp fungi:*
- 4: sp human:*
- 5: sp invertibrate:*
- 6: sp mammal:*
- 7: sp mhc:*
- 8: sp organelle:*
- 9: sp phage:*
- 10: sp plant:*
- 11: sp rodent:*
- 12: sp virus:*
- 13: sp vertebrate:*
- 14: sp unclassified:*
- 15: sp rvirus:*
- 16: sp bacteriaph:*
- 17: sp archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1528	87.6	330	2	Q8VU82	Q8VU82 mycobacteri
2	1515	86.8	330	2	Q8L371	Q8L371 mycobacteri
3	1162	66.6	352	2	Q8KY58	Q8KY58 mycobacteri
4	1106.5	63.4	349	2	Q8KY59	Q8KY59 mycobacteri
5	634	36.3	136	2	P71483	P71483 mycobacteri
6	621	35.6	139	2	Q9F7W5	Q9F7W5 mycobacteri
7	553	31.7	140	2	P71531	P71531 mycobacteri
8	544	31.2	136	2	P71519	P71519 mycobacteri
9	473	27.1	669	16	Q8FM00	Q8FM00 corynebacte
10	428.5	24.6	120	2	P72063	P72063 mycobacteri
11	415	23.8	341	16	Q8NLB1	Q8NLB1 corynebacte
12	404	23.2	360	16	Q8FLZ9	Q8FLZ9 corynebacte
13	346	19.8	96	2	P71536	P71536 mycobacteri
14	303.5	17.4	411	16	Q8NRL7	Q8NRL7 corynebacte
15	297.5	17.0	77	2	Q9R667	Q9R667 mycobacteri
16	284.5	16.3	390	16	Q8FT53	Q8FT53 corynebacte

17	279	16.0	462	16	Q8NEW9	Q8NRW9 corynebacte
18	277	15.9	483	16	Q8NNL2	Q8NNL2 corynebacte
19	263	15.1	358	2	Q93R90	Q93R90 corynebacte
20	260	14.9	52	2	Q9S6X0	Q9S6X0 mycobacteri
21	257.5	14.8	381	16	Q8FSM7	Q8FSM7 corynebacte
22	252	14.4	484	16	Q8FQY3	Q8FQY3 corynebacte
23	238.5	13.7	365	16	Q8NTG4	Q8NTG4 corynebacte
24	233.5	13.4	342	16	Q86543	Q86543 streptomyc
25	192	11.0	39	2	Q8R5J7	Q8R5J7 mycobacteri
26	167	9.6	50	2	Q93JZ6	Q93JZ6 mycobacteri
27	167	9.6	261	16	Q99ZYL	Q99ZYL streptococc
28	166	9.5	261	16	Q8P189	Q8P189 streptococc
29	156	8.9	37	2	Q9R5J5	Q9R5J5 mycobacteri
30	144.5	8.3	94	16	Q8VKB0	Q8VKB0 mycobacteri
31	143	8.2	259	16	Q97S09	Q97S09 streptococc
32	143	8.2	259	16	Q8DQR2	Q8DQR2 streptococc
33	138	7.9	58	2	O52955	O52955 mycobacteri
34	136	7.8	276	16	Q8P5F4	Q8P5F4 xanthomonas
35	134	7.7	252	16	Q928K5	Q928K5 listeria in
36	133	7.6	252	16	Q8Y4K5	Q8Y4K5 listeria mo
37	132	7.6	258	16	Q9L9X0	Q9L9X0 lactococcus
38	129.5	7.4	76	16	P71563	P71563 mycobacteri
39	127	7.3	258	2	Q9RAU7	Q9RAU7 lactococcus
40	126	7.2	288	5	Q8I1B5	Q8I1B5 drosophila
41	125	7.2	377	16	Q9X8H6	Q9X8H6 streptomyc
42	123.5	7.1	282	4	Q9BVJ2	Q9BVJ2 homo sapien
43	123	7.0	263	16	Q8DTB4	Q8DTB4 streptococc
44	121.5	7.0	258	2	Q8KWI9	Q8KWI9 lactococcus
45	121.5	7.0	278	2	O52299	O52299 anabaena az
46	121	6.9	276	16	Q8PPF0	Q8PPF0 xanthomonas
47	119.5	6.8	269	2	Q9E2Z5	Q9E2Z5 pasteurella
48	118.5	6.8	258	2	Q9L9W2	Q9L9W2 lactococcus
49	118.5	6.8	258	2	Q8KXE1	Q8KXE1 lactococcus
50	117.5	6.7	269	16	Q9CKZ9	Q9CKZ9 pasteurella
51	114.5	6.6	806	3	Q9P4T8	Q9P4T8 agaricus bi
52	113	6.5	282	6	Q9GJT2	Q9GJT2 sus scrofa
53	113	6.5	282	11	Q9R0P3	Q9R0P3 mus musculu
54	113	6.5	282	16	Q8YTB5	Q8YTB5 anabaena sp
55	113	6.5	312	11	Q9CWI4	Q9CWI4 mus musculu
56	112	6.4	272	10	Q8LAS8	Q8LAS8 arabidopsis
57	112	6.4	284	10	O22215	O22215 arabidopsis
58	111	6.4	322	16	Q8UDW6	Q8UDW6 agrobacteri
59	111	6.4	618	16	Q9A3F8	Q9A3F8 caulobacter
60	110.5	6.3	262	16	Q8DZC4	Q8DZC4 streptococc
61	110	6.3	282	6	Q9GM98	Q9GM98 sus scrofa
62	109.5	6.3	262	16	Q8E4Y4	Q8E4Y4 streptococc
63	109.5	6.3	577	2	Q9REI6	Q9REI6 arthrobacte
64	109	6.2	363	16	Q9RK16	Q9RK16 streptomyc
65	108	6.2	252	16	Q8DF76	Q8DF76 vibrio vuln
66	108	6.2	264	2	O31030	O31030 pectobacter
67	108	6.2	276	16	P73137	P73137 synchocyst
68	107.5	6.2	286	5	Q9VDP9	Q9VDP9 drosophila
69	107.5	6.2	689	16	Q8YU28	Q8YU28 anabaena sp
70	106	6.1	20	2	Q9R5R7	Q9R5R7 mycobacteri
71	105.5	6.0	293	16	Q99RU5	Q99RU5 staphylococ
72	105.5	6.0	293	16	Q8NV67	Q8NV67 staphylococ
73	105.5	6.0	415	16	Q9WX03	Q9WX03 streptomyc
74	105	6.0	430	16	Q9I739	Q9I739 pseudomonas
75	104	6.0	280	16	Q8ZG19	Q8ZG19 yersinia pe
76	104	6.0	578	2	Q8GRC2	Q8GRC2 marinobacte
77	104	6.0	963	3	O43024	O43024 schizosacch
78	103.5	5.9	277	16	Q8X5J5	Q8X5J5 escherichia
79	103.5	5.9	279	16	Q8EPC6	Q8EPC6 shewanella
80	103.5	5.9	596	16	Q8DLG3	Q8DLG3 synchococc
81	103	5.9	274	2	Q8GR67	Q8GR67 abiectophia
82	102.5	5.9	849	16	Q8PPH0	Q8PPH0 xanthomonas
83	101.5	5.8	277	16	Q92OE0	Q92OE0 rhizobium m
84	101.5	5.8	437	16	Q8DHQ9	Q8DHQ9 synchococc
85	101.5	5.8	510	5	O44018	O44018 leishmania
86	101	5.8	279	2	Q51671	Q51671 paracoccus
87	101	5.8	289	16	Q8YIT5	Q8YIT5 talstonia s
88	100.5	5.8	328	16	Q9A7U1	Q9A7U1 caulobacter
89	100	5.7	466	16	Q92LZ9	Q92LZ9 rhizobium m

O82950 pseudomonas

90 99.5 5.7 576 2 O82950

ALIGNMENTS

RESULT 1

Q8VU82 PRELIMINARY; PRT; 330 AA.
AC Q8VU82;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Fibronectin-binding antigen 85 complex B.
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-F., Shin K.-S.;
RT "Cloning and sequencing of gene encoding the antigen 85 complex B from
RL Mycobacterium paratuberculosis."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF219121; AAL56853.1; -. put.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
SQ SEQUENCE 330 AA; 34693 MW; 7E5C474F40C01001 CRC64;

Query Match 87.6%; Score 1528; DB 2; Length 330;
Best Local Similarity 85.5%; Pred. No. 2.8e-108;
Matches 277; Conservative 22; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDLSEKVRAGRRLLVGAATAVTLPGLLGAGGAATANAFSRPGLPVEYLQVPSMGR 60
Qy 61 DIKVFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFY 120
Db 61 DIKVFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFY 120
Qy 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
Db 121 DWYQACGKAGCSTYKWTETLTSELPSYLSNKGVRKTSAAVGLSMSSAMILAVNHP 180
Qy 181 QQFIYAGLSALLDPSQGMPSLIGLAWDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
Db 181 DQFIYAGLSALLDPSQGMPSLIGLAWDAGGYKADAMWGPSSDPAWQRNDPSLHPEL 240
Qy 241 VANNTRLWVYCGNGTPELGGANITPAEFLNFVRSSNLKFQDAYNAAGHNAVENFPNG 300
Db 241 VGHNTRLWVYCGNGTPELGGANITPAEFLNFVRSSNLKFQDAYNGAGHNAVENFNANG 300
Qy 301 THSWEYGAQLNAMKGLQSSIGA 324
Db 301 THSWEYGAQLNAMKPDQLGTGCA 324

RESULT 2

Q8L371 PRELIMINARY; PRT; 330 AA.
AC Q8L371;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE 85B protein.
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19698;

RX MEDLINE=22000114; PubMed=12005331;
RA Mullerad J., Bercovier H.;
RT "The immunogenicity of Mycobacterium paratuberculosis 85B antigen."
RL Med. Microbiol. Immunol. 190:179-184 (2002).
DR EMBL; AF389346; AAM21939.1; -.
SQ SEQUENCE 330 AA; 34823 MW; 00F8D0CF079084A8 CRC64;

Query Match 86.8%; Score 1515; DB 2; Length 330;
Best Local Similarity 84.9%; Pred. No. 2.7e-107;
Matches 275; Conservative 22; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDLSEKVRAGRRLLVGAATAVTLPGLLGAGGAATANAFSRPGLPVEYLQVPSMGR 60
Qy 61 DIKVFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFY 120
Db 61 DIKVFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFY 120
Qy 121 DWYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
Db 121 DWYQACGKAGCSTYKWTETLTSELPSYLSNKGVRKTSAAVGLSMSSAMILAVNHP 180
Qy 181 QQFIYAGLSALLDPSQGMPSLIGLAWDAGGYKAADMWGPSSDPAWERNPTQOIPKL 240
Db 181 DQFIYAGLSALLDPSQGMPSLIGLAWDAGGYKADAMWGPSSDPAWQRNDPSLHPEL 240
Qy 241 VANNTRLWVYCGNGTPELGGANITPAEFLNFVRSSNLKFQDAYNAAGHNAVENFPNG 300
Db 241 VGHNTRLWVYCGNGTPELGGANITPAEFLNFVRSSNLKFQDAYNGAGHNAVENFNANG 300
Qy 301 THSWEYGAQLNAMKGLQSSIGA 324
Db 301 THSWEYGAQLNAMKPDQLGTGCA 324

RESULT 3

Q8KY58 PRELIMINARY; PRT; 352 AA.
AC Q8KY58;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Antigen 85C complex.
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang Y.-F., Shin K.-S.;
RT "Cloning and characterization of Mycobacterium avium subsp.
RL paratuberculosis gene 85C."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF280068; AAM73518.1; -.
SQ SEQUENCE 352 AA; 37754 MW; 39FFD0D7183975A8 CRC64;

Query Match 66.6%; Score 1162; DB 2; Length 352;
Best Local Similarity 66.0%; Pred. No. 2.1e-80;
Matches 214; Conservative 40; Mismatches 64; Indels 6; Gaps 2;

Qy 6 RKIR----AWGRRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 61
Db 8 RKLGAATAATMPERLALAAVAGSLLSGVAAGGSPVAGAFSKPGLPVEYLEVPSMGRN 67
Qy 62 IKVFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFYSD 121
Db 68 IKVFQGGGPH--AVYLLDGLRAQDDYNGWDINTPAFEFQSGLSIVMPVGGSSFY 125
Qy 122 WYSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHPQ 181
Db 126 WYQPSGNGQNTYKWTETLTQEMPLMQSNKQVSPAGNAAGLSMSSGSSALIAAYYPQ 185

QY 182 QTYAGSLSDLPSCMGPSLIGLAWDAGGYKAADMWGPSSDPAWERNNDPTQOIPKLV 241
 Db 186 QFYAASLSGFLNPSGFWPTLLGLAWDSGGYNANSMWGPSTDPKAKRNDPMVQIPRV 245
 QY 242 ANNTRLWVYCGTNPNEGANIPAFLENFVRSSNLKFQDAYNAAGGHNAVFPNPGT 301
 Db 246 ANNTRIWVYCGTNPNEGANIPAFLENTLRTNEQFONNYAAGRGVNFPPANGT 305
 QY 302 HSWYVWGAOLNANKDGLQSSLGAG 325
 Db 306 HSWPYWQOLMAKPKDMQOVLLSG 329

RESULT 4

Q8KY59 PRELIMINARY; PRT; 349 AA.
 AC Q8KY59;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DE 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 OS Antigen 85A complex.
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chang Y.-F., Shin K.-S.;
 RT "Cloning and characterization of Mycobacterium avium subsp.
 paratuberculosis gene for 85A."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF280067; AAM73517.1; --
 SQ SEQUENCE 349 AA; 36763 MW; E3EB5DDDDACCSC085 CRC64;

Query Match 63.4%; Score 1106.5; DB 2; Length 349;
 Best Local Similarity 64.0%; Pred. No. 3.4e-76;
 Matches 219; Conservative 34; Mismatches 58; Indels 31; Gaps 7;

QY 1 MTDVSR---KIRAWGRRLMTGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVSPS 57
 Db 1 MTLVDRLGAVAGMPRLVGVAGGALLSLGLGAVGSGATAGAFSRPGLPVEYLQVPSAA 60
 QY 58 MGRDIKVFQSGGNSPAVYLLDGLRADDDYNGWDINTPAFEWYQSGLSIVMPVGQSS 117
 Db 61 MGRDIKVFQSGGNSPALYLLDGMRAQDDFNWDINTPAFEWYQSGLSIVMPVGQSS 120
 QY 118 FYSDWYSPACGKAGCQTYKWTFTLSELPWLSANRAVKPTGSAAGLSMAGSSAMIL-- 175
 Db 121 FYSDWYKPCGKAGCTYKWTFTLSELPYLSAQKQVKPTGSGVGL-----ADGRLLR 176
 QY 176 ---AAYHPQOFIYAGLSALLD-PSQMGPSLIGLAWG-----DAGGYKAADMWGPSS 224
 Db 177 LSWAATTPQFVYAGLSALLVELVARAWARRLLGLAMGTPTVATRPPTCGVRRRTREGPAT 236
 QY 225 DPAWERNNDPTQOI--PKLVANNTRLWVYCGTNPNEGANIPAFLENFVRSSNLKFQD 282
 Db 237 -----TTRCRSASLVANNTRIWVYCGNGKPSDLGGDNLPAKLELGFVRTSNLKFQD 287
 QY 283 AYNAGGHNAVNFPPNGTHSYWGAQNALNMGKDLQSSILGA 324
 Db 288 AYNAGGHNAVNFNDANGTHDPYWGALQKAMKPDQLQSLVGA 329

RESULT 5

P71483 PRELIMINARY; PRT; 136 AA.
 ID P71483;
 AC P71483;
 DT 01-FEB-1997 (TremBLrel. 02, Created)
 DT 01-FEB-1997 (TremBLrel. 02, Last sequence update)
 DE 01-DEC-2001 (TremBLrel. 19, Last annotation update)
 OS 32-Kda protein (fragment).
 OS Mycobacterium asiaticum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1790;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25276;
 RX MEDLINE=97193847; PubMed=9041432;
 RA Soinali H.K., Viljanen M.K.;
 RT "Diversity of the 32-kDa protein gene may form a basis for species
 determination of potentially pathogenic mycobacterial species."
 RL J. Clin. Microbiol. 35:769-773 (1997).
 DR EMBL; Y07715; CAA68987.1; --
 DR HSSP; P31953; 1DQZ.
 DR InterPro; IPR000801; Esterase_put.
 DR Pfam; PF00756; Esterase; 1.
 FT NON_TER 1
 FT NON_TER 136
 SQ SEQUENCE 136 AA; 14504 MW; DF1071EA4B700B42 CRC64;

Query Match 36.3%; Score 634; DB 2; Length 136;
 Best Local Similarity 83.1%; Pred. No. 8.4e-41;
 Matches 113; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 119 YSDWYSPACGKAGCQTYKWTFTLSELPWLSANRAVKPTGSAAGLSMAGSSAMILAA 178
 Db 1 YSDWYNAGCGKAGWTYKWTFTLSELPAYLSSNKQVKPTGSAAGLSMAGSSAMILAA 60
 QY 179 HPQOFIYAGLSALLDPSQMGPSLIGLAWDAGGYKAADMWGPSSDPAWERNNDPTQOIP 238
 Db 61 HPQOFIYAGLSALLDPSQMGPSLIGLAWDAGGYKASDMWGPKEDEFAWQRNDSLQVS 120
 QY 239 KLVANNTRLWVYCGNG 254
 Db 121 RLVANNTRLWVYCGNG 136

RESULT 6

Q9F7W5 PRELIMINARY; PRT; 139 AA.
 ID Q9F7W5;
 AC Q9F7W5;
 DT 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DE 01-JUN-2002 (TremBLrel. 21, Last annotation update)
 DE Putative 32 kDa surface antigen (Fragment).
 GN FBPA.
 OS Mycobacterium ulcerans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1809;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19423;
 RX MEDLINE=20507800; PubMed=11053375;
 RA Steinar T.P., Jenkin G.A., Johnson P.D., Davies J.K.;
 RT "Comparative genetic analysis of mycobacterium ulcerans and
 mycobacterium marinum reveals evidence of recent divergence."
 RL J. Bacteriol. 182:6322-6330 (2000).
 DR EMBL; AF271092; AAG31743.1; --
 DR HSSP; P31953; 1DQZ.
 DR InterPro; IPR000801; Esterase_put.
 DR Pfam; PF00756; Esterase; 1.
 FT NON_TER 1
 FT NON_TER 139

SQ SEQUENCE 139 AA; 14431 MW; 68A4138016622CF7 CRC64;
 Query Match 35.6%; Score 621; DB 2; Length 139;
 Best Local Similarity 79.9%; Pred. No. 8.4e-40;
 Matches 111; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 157 PTGSAAGLSMAGSSAMILAAVHPQOFIYAGLSALLDPSQMGPSLIGLAWDAGGYKA 216
 Db 1 PTGSGVGLSMAGSSAMILAAVHPQOFIYAGLSALLDPSQMGPSLIGLAWDAGGYKA 60
 QY 217 ADMWGPSSDPAWERNNDPTQOIPKLVANNTRLWVYCGTNPNEGANIPAFLENFVRSS 276


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QY 297 PPNCTHSHWYCAQLNANKGDLQSSLG 323
Db 371 RPSGVHAWPYQFQEMTQAWPYNADSLG 397

RESULT 10
P72063 PRELIMINARY; PRT; 120 AA.
ID P72063
AC P72063;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 32-kDa protein (Fragment).
OS Mycobacterium vaccae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1810;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29678;
RX MEDLINE=97193847; PubMed=9041432;
RA Soini H.K., Viljanen M.K.;
RT "Diversity of the 32-kDa protein gene may form a basis for species
RT determination of potentially pathogenic mycobacterial species.";
RL J. Clin. Microbiol. 35:769-773 (1997).
DR EMBL; Y07719; CAA68991.1; -.
DR HSSP; P31953; 1DQZ.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
FT NON_TER 1 120
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13279 MW; BA935A7A28C36374 CRC64;

Query Match 24.6%; Score 428.5; DB 2; Length 120;
Best Local Similarity 65.0%; Pred. No. 3e-25;
Matches 78; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

QY 136 KWETFLTSELPOWLSANRAVPTGSAIGLSMAGSSAMILAAHYHPQOFIYAGSLALLDP 195
Db 1 KWETFLTQELPYLQXNKGVDPENRAGVLSMAGSSPVTLAIYHPQOFQYAGSLGYLNL 60

QY 196 SOGMPSLIGLAMDAGGYKAADMWGPS-SDPAMERNPTQOIIPKLVANNTRLVYCGNG 254
Db 61 SEGWWFVLNISMGDAGGYDANDMWGPAETDPAWQYNDPMVQIPRLVANNRVRVYCGNG 120

RESULT 11
Q8FLZ9 PRELIMINARY; PRT; 341 AA.
ID Q8FLZ9
AC Q8FLZ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Predicted esterase.
GN CGL2878.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005283; BAC00272.1; -.
DR InterPro; IPR000801; Esterase_put.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00756; Esterase; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
KW Complete proteome.
SQ SEQUENCE 341 AA; 37187 MW; 91877B75D835BE94 CRC64;

Query Match 23.8%; Score 415; DB 16; Length 341;
Best Local Similarity 33.7%; Pred. No. 1.3e-23;
Matches 116; Conservative 52; Mismatches 142; Indels 34; Gaps 9;

QY 3 DVSRKIRAWGRRLMIGTAAAVLPLGLVGIAGATAGAFSRP-----GLP 47
Db 9 EASRKLVA-----LVVALATAAAL-----MVVGQGTAAQANRDWLRADNSGYCDWDVAVGFW 59

QY 48 VEYLQVPSMGRIKQVQSGGNNSPA-VLLDGLRAQDDYNGWDINTPAFEWYQSG 106
Db 60 VQRCDDVSPAMGRNIPVQIQPAGGAGNAGLVLLDGMGRATEYSNAWLVDTNARLYAPNNI 119

QY 107 SIVMPVGQSSFFSYSDWYSPA-CGKAGCQTYKWETFLTSELPOWLSANRAVPTGSAATGL 165
Db 120 TLVMPVGAGSFYADWMSQASLSSDPVIYWEFTLQELPAYLEQNGFVARNNNSIGL 179

QY 166 SMAGSSAMILAAHYHPQOFIYAGSLALLDPSQGMGPSILGLAMGDAGGYKAADMWGPS 225
Db 180 SMGGTAALNLAAKHPDQFQAMSWSGYINTTAPGMQTLRLMLDLDTGGFNVNMYGSIIN 239

QY 226 PAWERNPTQOIIPKLVANNTRLVYCGNG--TPNELG---GANIPAELENFVRSSNLKF 280
Db 240 PRRENDFPNWNGGLA--NTDVLISAASGLWSPQDDGVVRDHRDTGVSYLE-FVAMTSTRI 296

QY 281 QDAYNAAAGHNAVFNPFPNGTHSWYGAQLNANKGDLQSSLG 324
Db 297 WEAKARLQGLNPTADYPMYGLHGWAFNSQLERLQGRVLDVMA 340

RESULT 12
Q8FLZ9 PRELIMINARY; PRT; 360 AA.
ID Q8FLZ9
AC Q8FLZ9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative P51 protein.
GN CR2710.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kwarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Ueda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005223; BAC19520.1; -.
KW Complete proteome.
SQ SEQUENCE 360 AA; 39009 MW; A2AFF89D8D7C4619 CRC64;

Query Match 23.2%; Score 404; DB 16; Length 360;
Best Local Similarity 34.1%; Pred. No. 9.4e-23;
Matches 118; Conservative 51; Mismatches 137; Indels 40; Gaps 10;

QY 4 VSRKIRAWGRRLMIGTAAAVLPLGLVGIAGATAG--AFSRP-----GLPVEY 50
Db 29 VSHKLLA-----LVVALATAA--GLMVVGTTGAQAANRDWLRDPDSTGHCDWDGVYVQR 81

QY 51 LQVPSMGRIKQVQSGGNNSPA-VLLDGLRAQDDYNGWDINTPAFEWYQSG 107
Db 82 CDVYSPAMGRNIAVQIQPAGGAGN--AGLYLDGMGRATEYSNAWLVDTNARLYAPNNI 139

QY 108 SIVMPVGQSSFFSYSDWYSPA-CGKAGCQTYKWETFLTSELPOWLSANRAVPTGSAATGL 166
Db 140 LVMPVGAGSFYADWMSQASLSSDPVIYWEFTLQELPAYLEQNGFVARNNNSVAGLS 199

QY 167 MAGSSAMILAAHYHPQOFIYAGSLALLDPSQGMGPSILGLAMGDAGGYKAADMWGPS 226
Db 167 MAGSSAMILAAHYHPQOFIYAGSLALLDPSQGMGPSILGLAMGDAGGYKAADMWGPS 226

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Db 200 MGGTAALNLAAKHPQFRQAMSYSGYLTTTAPGCMQMLRLAMLDGTGGFNVMAMVGSVINP 259
QY 227 AWERNDPQOQPKL-----VANTRLWVYCGNT--PNELGGANIPAEFLNFVRSSNL 278
Db 260 RRFENDPFNNWGLRGKDVVYSAASGLWGPQDNGTRVDRHNGSVLEA-----VSLATT 313
QY 279 KFQDAYNAAGHNVAFFNPPNGTSHWYWGALNMGKDLQSSLGA 324
Db 314 PAWEKARAEGLNVTADYPTNGIHSWAQFSSQLHKTRDRVLNVMA 359

RESULT 13
P71536
ID P71536 PRELIMINARY; PRT; 96 AA.
AC P71536;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE 32-kDa protein (Fragment).
OS Mycobacterium triviale.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1798;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23291;
EX MEDLINE=97193847; PubMed=9041432;
RA Soini H.K., Viljanen M.K.;
RT "Diversity of the 32-kDa protein gene may form a basis for species
determination of potentially pathogenic mycobacterial species.";
RL J. Clin. Microbiol. 35:769-773 (1997).
DR EMBL: Y07716; CAA68988.1; -.
DR HSSP: P31953; 1DQZ.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10206 MW; 52PB7E4708FBA85E CRC64;

Query Match 19.8%; Score 346; DB 2; Length 96;
Best Local Similarity 61.5%; Pred. No. 4.2e-19;
Matches 59; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

QY 159 GSAALGLSMAGSSAMILAAHYHPQFIYAGSLALLDPSQGMGSPSLIGLAMGDAGYKAAD 218
Db 1 GNAVVLGSMGSGTATYAIWHPEQAFAGSLSGFLNPSNGWWPTLLIGFAMKDDAGFNGTD 60

QY 219 MWGSSDPAWERNPTQOIPKLVANTRILWVYCGNG 254
Db 61 MWGPAADVAWRNDPTVANVARLVANTRVWVYCGNG 96

RESULT 14
Q8NRL7
ID Q8NRL7 PRELIMINARY; PRT; 411 AA.
AC Q8NRL7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Hypothetical protein Cg11031.
GN CGL1031.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005277; BAB98424.1; -.
DR InterPro; IPR000801; Esterase_put.

DR InterPro; IPR000379; Ser_estr_site.
DR Pfam; PF00756; Esterase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 411 AA; 43660 MW; B9ABBC09B501FE3 CRC64;

Query Match 17.4%; Score 303.5; DB 16; Length 411;
Best Local Similarity 30.2%; Pred. No. 4.9e-15;
Matches 86; Conservative 49; Mismatches 121; Indels 29; Gaps 10;

QY 45 GLPVEYLQVPSMGRDIKVQ-FQSGNNNSPA--VYLLDGLRAQDDYNGWDINTPAFEW 101
Db 126 GLRLKSVASPSMQRNVDVQIMKSAREADSPAPMLYMLDGGKNNKSSGNGGEGPKVF 185
QY 102 YQSGLSIVMPVGGOSFYSDWY--SPACGKAGCQTYKWETFTLTSELPOWLSANRAVKPTG 159
Db 186 ADENVTVVMPGLCAASSYSDWLEEDPALGR-----IKWETFIVELEAPLLAEAREELNFG 240
QY 160 SAAI-GLSMAGSSAMILAAHYHPQF---IYAGSLALLDPSQGMGSPSLIGLAMGDAGYK 215
Db 241 HRGIGLSMGATGAVHLANSNPDLFDGVIGISGCVSTLDP---IGQTTVSLIVNSRGG-N 296

QY 216 AADMWGSSDPAWERNPTQOIPKLVANTRILWVYCGNGTNELGGANIPAE----- 267
Db 297 VENMWGPTGSETWKAHDVTSNPEGL--RDMAYVLSAANGVVDIDLADSEKEPFYNLLAG 354

QY 268 -FLENFVRSNLLKFQDAYNAAGHNVAFFNPPNGTSHWYWGAL 311
Db 355 VLERGSLSCTEALDESNRAGNHQVVDYKDSGTHINWNPQL 399

RESULT 15
Q9R667
ID Q9R667 PRELIMINARY; PRT; 77 AA.
AC Q9R667;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Antigen 85B=SECRETED protein (Fragments).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
EX MEDLINE=92366936; PubMed=1502498;
RA Wiker H.G., Nagai S., Harboe M., Ljungqvist L.;
RT "A family of cross-reacting proteins secreted by Mycobacterium
tuberculosis.";
RL Scand. J. Immunol. 36:307-319 (1992).
DR HSSP: P31953; 1DQY.
FT NON_TER 1
FT NON_TER 41
FT NON_TER 42
FT NON_TER 77
SQ SEQUENCE 77 AA; 8385 MW; C1802000ED3B1515 CRC64;

Query Match 17.0%; Score 297.5; DB 2; Length 77;
Best Local Similarity 28.8%; Pred. No. 1.5e-15;
Matches 75; Conservative 0; Mismatches 2; Indels 183; Gaps 1;

QY 41 FSRPGLPVEYLQVPSMGRDIKVQFQSGNNNSPAVYLLDGLRAQDDYNGWDINTPAFEW 100
Db 1 FSRPGLPVEYLQVPSMGRDIKVQFQSGNNNSPAVYLLDG----- 41

QY 101 YQSGLSIVMPVGGOSFYSDWYSPACGKAGCQTYKWETFTLTSELPOWLSANRAVKPTG 160
Db 42 ----- 41

QY 161 AAIGLSMAGSSAMILAAHYHPQFIYAGSLALLDPSQGMGSPSLIGLAMGDAGYKAADMW 220
Db 42 ----- 41

QY 221 GPSSDPAWERNPTQOIPKLVANTRILWVYCGNGTNELGGANIPAEFLNFVRSSNLKF 280
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Db 42 -----PABFLENFVRSSNLKP 57
QY 281 QDAYNAGGHNAVFPPNG 300
Db 58 QDAYKPGAGHNAVFPPNG 77

RESULT 16
Q8FTS3
ID Q8FTS3 PRELIMINARY; PRT; 390 AA.
AC Q8FTS3;
DT 01-OCT-2003 (TREMBlrel. 23, Created)
DT 01-OCT-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 23, Last annotation update)
DE Putative PSI protein.
GN CE1488.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005219; BAC18298.1; -.
KW Complete proteome.
SQ SEQUENCE 390 AA; 41356 MW; 46C3B7B47B08DBF8 CRC64;

Query Match 16.3%; Score 284.5; DB 16; Length 390;
Best Local Similarity 28.6%; Pred. No. 1.3e-13;
Matches 83; Conservative 46; Mismatches 122; Indels 39; Gaps 10;

QY 45 GLPVEYLQVPSMGGRDIKVOFQ---SGNNSPAVLLDGLRAQDDYNGWDINTPAFEWY 101
Db 105 GLRLERWTVASPSMQRNVDVQIMRSVDAGAPAPMLYLDIGIGNRNNSGWINHGQGPKEV 164
QY 102 YQSGLSIVMPVGGQSFYSWDY--SPACGKAGCQTYKWTFTLSELTPQWLSANRAVKPTG 159
Db 165 GENVIVVMPGLGAASMYSDWEEDPALGR-----IWWETFIIVEELAPLLEAEELFNFG 219
QY 160 SAAI-GLSMAGSSAMILAAHYHPOQF---IYAGLSALLDPSQGMGPSLIGLAMGDAGYK 215
Db 220 HRGIGGLSGCATGAVHLANANPDFFDAVIGISCYSTLDP---IGQATVSLIVKSRG-D 275
QY 216 AADMWGPSSDPAPERNDPQQIPKLVAN-----NTRLWYCGNGTNELGGANIPAEFLE 270
Db 276 VENMWGPVGSRTWQEHQ-----VVSNPEGLNMAVLSAANGVVDEIDREYADEPFY 328
QY 271 NFVRSNLK-----FQDAYNAAGGHNAVFPPNGTHSWEYGAQL 311
Db 329 NLLAGTVLBERGALSCTEALDDAQMDQAGTHQVVDYKAGAHNRNFEQL 378

RESULT 17
Q8NRW9
ID Q8NRW9 PRELIMINARY; PRT; 462 AA.
AC Q8NRW9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein Cg10922.
GN Cg10922.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1716;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

Query Match 15.9%; Score 277; DB 16; Length 483;
Best Local Similarity 28.9%; Pred. No. 6.3e-13;
Matches 82; Conservative 43; Mismatches 133; Indels 26; Gaps 9;

QY 48 VEYLQVPSMGGRDIKVOFQSGNNS---PAYLLDGLRAQDDYNGWDINTPAFEWYQS 104
Db 129 IRQINAYSPSMGRITPLVWVVPEDNTVPQPTVYALGGDGGQGNWVTRTDLDELTSN 188
QY 105 GLSIWMPVGGQSFYSWDYSPACGKAGCQTYKWTFTLSELTPQWLSANRAVKPTGSAAI- 163
Db 189 NINLIMPMLGSPSFYADWAGESSEMGGAQ--QWETFLMHELPELEA--AIGADGORSIV 244
QY 164 GLSMAGSSAMILAAHYHPOQFIYAGLSALLDPSQGMGPSLIGLAMGDAGYKAADMWGPS 223
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;

Query Match 16.0%; Score 279; DB 16; Length 462;
Best Local Similarity 28.9%; Pred. No. 4.2e-13;
Matches 82; Conservative 44; Mismatches 132; Indels 26; Gaps 9;

QY 48 VEYLQVPSMGGRDIKVOFQSGNNS---PAYLLDGLRAQDDYNGWDINTPAFEWYQS 104
Db 108 IRQINAYSPSMGRITPLVWVVPEDNTVPQPTVYALGGDGGQGNWVTRTDLDELTSN 167
QY 105 GLSIWMPVGGQSFYSWDYSPACGKAGCQTYKWTFTLSELTPQWLSANRAVKPTGSAAI- 163
Db 168 NINLIMPMLGSPSFYADWAGESSEMGGAQ--QWETFLMHELPELEA--AIGADGORSIV 223
QY 164 GLSMAGSSAMILAAHYHPOQFIYAGLSALLDPSQGMGPSLIGLAMGDAGYKAADMWGPS 223
Db 224 GMSMGSGSVINPETHDPNIFYSSVSGSAGCAETNSWMGRR--GIATAYNGNVVPEQIFGE 281
QY 224 SDPAWER-NDPTQQIPKLVANNTRLWVYCGNGTNPSELG--GANIPAE-----F 268
Db 282 VDSYDSRYNDPLNAAKL--EQDNLVIFAGSGVSELDVIGNAPIDEADAFKRVLVGFE 340
QY 269 LENFVRSSNLKFDQDAYNAAGGHNAVFPPNGTHSWEYGAQLN 312
Db 341 IEAMSNCTCHNLKAATDQMGIDNINYDFRPTGTHAWDYWNEALH 384

RESULT 18
Q8NNL2
ID Q8NNL2 PRELIMINARY; PRT; 483 AA.
AC Q8NNL2;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein Cg12181.
GN Cg12181.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005280; BAB99574.1; -.
DR InterPro; IPR000801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 483 AA; 51567 MW; 8449C06238D83230 CRC64;

Query Match 15.9%; Score 277; DB 16; Length 483;
Best Local Similarity 28.9%; Pred. No. 6.3e-13;
Matches 82; Conservative 43; Mismatches 133; Indels 26; Gaps 9;

QY 48 VEYLQVPSMGGRDIKVOFQSGNNS---PAYLLDGLRAQDDYNGWDINTPAFEWYQS 104
Db 129 IRQINAYSPSMGRITPLVWVVPEDNTVPQPTVYALGGDGGQGNWVTRTDLDELTSN 188
QY 105 GLSIWMPVGGQSFYSWDYSPACGKAGCQTYKWTFTLSELTPQWLSANRAVKPTGSAAI- 163
Db 189 NINLIMPMLGSPSFYADWAGESSEMGGAQ--QWETFLMHELPELEA--AIGADGORSIV 244
QY 164 GLSMAGSSAMILAAHYHPOQFIYAGLSALLDPSQGMGPSLIGLAMGDAGYKAADMWGPS 223
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
```

Db 245 GMSGSGVLNFAITHDNFYSSVSGCAETNSWMCRR--GIAATAYNGNVVPEQIFGE 302
QY 224 SDPAWER-NDEPTQIPLKLVANNTELWYCGTGNELG--GANIPAE-----F 268
Db 303 VDSYRYNDPLNNAKL-EQDNLXIFAGSGVSELDVIGDNAPIDEDAFKKNVLVQFE 361
QY 269 LENFVRSNLKFDQAYNAAGHNAVFPPNPGTHSWYWGQALN 312
Db 362 IEAMSNCTHMLKAATQMGIDNINYDFRPTGTHAWDYNEALH 405

RESULT 19
Q93R90
ID Q93R90 PRELIMINARY; PRT; 358 AA.
AC Q93R90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Surface layer protein A.
GN SLPA.
OS Corynebacterium ammoniagenes (Brevibacterium ammoniagenes).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1697;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 6872;
RA Usuda Y., Kawasaki H., Utagawa T.;
RT "Characterization of a surface layer protein of Corynebacterium
ammoniagenes ATCC 6872.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB05224; BAB62413.1; -
DR InterPro; IPR000801; Esterase_cat.
DR Pfam; PF00756; Esterase; 1.
FT CHAIN 26 358
SQ SEQUENCE 358 AA; 39081 MW; 0785CA6602351A1C CRC64;

Query Match 15.1%; Score 263; DB 2; Length 358;
Best Local Similarity 27.5%; Pred. No. 4.9e-12;
Matches 81; Conservative 46; Mismatches 130; Indels 38; Gaps 10;

QY 51 LQVPSPM-GRDIKVFQSGGN-NSPAVLLDGLRAQDYNGWDINTPAFVWYQSLGI 108
Db 69 LQATSPAMDGRKVLAIIRAQNPDRPTIYLLNGAGSBDTDLNQSEAVDFYADKQNV 128
QY 109 VMPVGGSSFFSDWSPACGACGCTYKWFELTSELPOWLSANRAVPTCSAALGSLMA 168
Db 129 VIPQAGAFSYTDNTTTPNKSYLKGPKQWETFLTKELFGLPE-ERLQSNKRAIAGMSMS 187
QY 169 GSSAMILAAVHPQOFIVAGSLSALLDPQGMGSPSLIGLAMDAGGYKAADMWGSPSDFAW 228
Db 188 ATSSILLIAHQNGFYDVGVSAGCAGTSTPEYEAMRLTVNRGG-EPEQMWKMGSRTN 246
QY 229 ERNDPTQIPLKLVANNTELWYCGTGNELGGANIPAEFLN-----FVRSNLKQF 281
Db 247 RYNDALLNSDKL---RGTYLYSSGNLPGE---TDMPSYTKQGVDPDTTASVGAATLQIE 301
QY 282 DAYNAAG---GHN-----AVENFPNCTHSHWYWGQALNMGKQLQSS 321
Db 302 GGIETAGVNHCTHNLKAKLKSQNTPAIYFRDTGTHSWPGW-----REDLEKS 349

RESULT 20
Q9S6X0
ID Q9S6X0 PRELIMINARY; PRT; 52 AA.
AC Q9S6X0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha antigen, antigen 85B, MPB59, antigen 6 precursor
(Fragment).
OS Corynebacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG Tokyo;
RX MEDLINE=88314872; PubMed=2842287;
RA Matsuo K., Yamaguchi R., Yamazaki A., Tasaka H., Yamada T.;
RT "Cloning and expression of the Mycobacterium bovis BCG gene for
extracellular alpha antigen.";
RL J. Bacteriol. 170:3847-3854(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG Tokyo;
RX MEDLINE=98070721; PubMed=9405208;
RA Ohara N., Nishiyama T., Ohara-Wada N., Matsumoto S., Matsuo T.,
Yamada T.;
RT "Characterization of the transcriptional initiation regions of genes
for the major secreted protein antigens 85C and MPB51 of Mycobacterium
bovis BCG.";
RL Microb. Pathog. 23:303-310(1997).
DR EMBL; D78142; BAA11219.1; -
KW Signal.
FT SIGNAL 1 40 POTENTIAL.
FT CHAIN 41 >52 ALPHA ANTIGEN, ANTIGEN 85B, MPB59,
ANTIGEN 6.
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 5324 MW; 4DB001D1DF9CB082 CRC64;

Query Match 14.9%; Score 260; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQ 52
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQ 52

RESULT 21
Q8FSM7
ID Q8FSM7 PRELIMINARY; PRT; 381 AA.
AC Q8FSM7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN C03356.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005215; BAC17186.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 381 AA; 41563 MW; 5629AF5EFDCE79BE CRC64;

Query Match 14.8%; Score 257.5; DB 16; Length 381;
Best Local Similarity 25.5%; Pred. No. 1.4e-11;
Matches 93; Conservative 45; Mismatches 166; Indels 61; Gaps 13;

QY 13 RLRMIGTAA-----AVVLEPLGLVLA--GGAATAGAFSRPGLPV--EYLQVP----- 54
Db 18 RRAPAAALGIALSTVAPTAVSAALTPAAVAGDTPQSTITVGAKYPEQAPRWRARV 77
QY 55 -----SPSMGRDIK---VQFQSGNNSPAVLLDGLRAQDYNGWDINTPAF 98
Db 78 NASGERVKEMWAYSPSMGRDRLVVLVITADESAGRPRIYLLNGDGGEGGNANWIMQTDVI 137

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QY 99 EMYOSGLSIVMGSSQSFYDWYSPACGKAGCQTYKWTETLSELTPQLWLSANRAVKPT 158
Db 138 DYLEKXNVNVLPMGKFSYTDWQENNALGGKQ--MWETFLVKELPGPL--EBELNAD 193
QY 159 GSAAT-GLSMAGSSAMILAAHPOQFIYAGSLSLDPSQGMPSLIGLWGDAGYKAA 217
Db 194 GQRAIAGMSMATSLLPQHPYGFYDAAASFGSCASTSQPLPWEYIRLT--DRGNATPE 252
QY 218 DMWGSSDPANRNDPTQOIPKLIVANTRLWYCGNGTPELGGANIP-----AEFLE- 270
Db 253 QMWGPRGGEVNIYNDALNSDKL--RGTDLYISNASGLAGHESANSFENGLDQAYLSL 310
QY 271 -----NFRSSNLKFQDAYNAAGGNV---FNEPPNGTHSWEYWGQALNMGKDL 318
Db 311 AMTETIVTGGLEIATNKTCHDLKAKLDHAGIPADWNLRTPTGTHSGWQDDLRGSDWTF 370
QY 319 QSSLG 323
Db 371 ARSFG 375

RESULT 22
Q8FQY3
ID Q8FQY3 PRELIMINARY; PRT; 484 AA.
AC Q8FQY3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Putative surface layer protein.
GN CE0984.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005217; BAC17794.1;
KW Complete proteome.
SQ SEQUENCE 484 AA; 51867 MW; 5DF15F5A933478EB CRC64;

Query Match 14.4%; Score 252; DB 16; Length 484;
Best Local Similarity 28.4%; Pred. No. 5.1e-11;
Matches 82; Conservative 42; Mismatches 135; Indels 30; Gaps 10;

QY 45 GLPVEYLQVPSMGRIKVF---QSGGNNSPAVYLLDGLRAQDDYNGWDINTPAPEWY 101
Db 122 GERIQINAYSPMERWIPLVWIVPDTSEPRPLYALGGDGGQSSANNITKTDPELM 181
QY 102 YQGLSLTVMVGGSSPYDWYSPACGKAGCQTYKWTETLSELTPQLWLSANRAVKPTGS- 160
Db 182 SSNNHVIMPLGSHGFADWBEVNDLSLGGKQ--QWETFLTHPEPLEA--AIGGDGQR 237
QY 161 AATGLSMAGSSAMILAAHPOQFIYAGSLSLDPSQGMPSLIGLWGDAGYKAAADWW 220
Db 238 SLIGMSGGSVNIAHQNFVSSVNASLSGCAETSWMGRGVA-ATVYSGNATPTQIF 296
QY 221 GPSDDPANNERNDPTQOIPKLIVANTRLWYCGNGTPELGG--GANIP----- 265
Db 297 GEVDSYARYNDPVINAHRL-AQKDNLVYFAAGSVWSEVDVEGENAPEDEKGLKNRITVG 355
QY 266 --AEFLENFRSSNLKFQDAYNAAGGNV---FNEPPNGTHSWEYWGQALN 312
Db 356 FRIEALSN-TCTHNLKAADTYH--GIDTIHYDFRPTGTHAWDYNEALH 401

RESULT 23

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Q8NTG4
ID Q8NTG4 PRELIMINARY; PRT; 365 AA.
AC Q8NTG4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein Cgl0343.
GN CGL0343.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005275; BAB97736.1;
DR InterPro; IPR000801; Esterase_1.
DR Pfam; PF00756; Esterase_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 365 AA; 39506 MW; 57A7BF984A60D6C CRC64;

Query Match 13.7%; Score 238.5; DB 16; Length 365;
Best Local Similarity 26.9%; Pred. No. 3.7e-10;
Matches 78; Conservative 42; Mismatches 133; Indels 37; Gaps 10;

QY 55 SPSMGRIK---VOFGGNNSPAVYLLDGLRAQDDYNGWDINTPAPEWYQSGLSIYMP 111
Db 78 SPSMDRNVPLVITADESAGRPVYILLNGDGGGGAANWVMTDLDFYLEKXNVNVI 137
QY 112 VGGSSFYSDWYSPACGKAGCQTYKWTETLSELTPQLWLSANRAVKPTGSAI-GLSMAGS 170
Db 138 MEGKFSYTDWVENASLGGKQ--MWETFLVKELPGPL--EELNTDQORAIAGMSKAT 193
QY 171 SAMILAAHPOQFIYAGSLSLDPSQGMPSLIGLWGDAGYKAAADWWGPSDDPAWER 230
Db 194 TSLILFPQHPFGFYDAAASFGSCATSSLLPWEYIKLTL-DRGNATPQMGPRGGEYNIY 252
QY 231 NDPTQOIPKLIVANTRLWYCGNGTPELGGANIP-AEFLNFRSSNLK-----FQ 281
Db 253 NDALINSDKL--RGTELYVSNASGLAGWESVDSRPEGLNQVQSIAMAEVTVTGGIIE 310
QY 282 DAYNA-----AGHNAVENFPNCTHSWEYWGQALNMGKDLQSS 321
Db 311 AATNKCTHDLKAKLDSAGIPADWNLRTPTGTHSGW--QDDLRS 353

RESULT 24
O86543
ID O86543 PRELIMINARY; PRT; 342 AA.
AC O86543;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Putative secreted protein.
GN SCO6609 OR SC1F2.06.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]

```

SEQUENCE FROM N.A.
RC STRAIN=A3 (2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3 (2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Markle L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
RL EMBL: AL039128; CAA20497.1; -.
DR InterPro; IPR000801; Esterase_put.
DR InterPro; IPR000379; Ser_estrif_site.
DR Pfam; PF00756; Esterase; 1.
KW Complete proteome.
SO SEQUENCE 342 AA; 37450 MW; 1FA7C5635BB21435 CRC64;

Query Match	13.4%;	Score	233.5;	DB	16;	Length	342;	
Best Local Similarity	28.2%;	Pred. No.	8.1e-10;					
Matches	100;	Conservative	46;	Mismatches	134;	Indels	75;	
Gaps	21;							
QY	15	LMIGTAAAVLPL	GLVGLAGGAATAGAFSRPGLPVEY	-----	LQVPSPM-GRDI	62		
Db	18	LVLAVLLAVLTP	TAPELALAGKPTGA	-TRHGAEVAVTRVAD	ROVDLTVRSTALGRTV	76		
QY	63	KVQF	-----	NSPVAYLDDGLRAQDDYDNG	DINTAFEFWYOSGLS	112		
Db	77	EVRLITPDGWN	PHDRRHQWPTLWLLHG	---CCGDTYSWTSMTD	VAETESLRDLVAVMPE	134		
QY	113	GQGSFYS	DYDWSPACGKAGCCTYKWEFLTSELQOWL	-----	SANRAVKFTGSAALGLS	166		
Db	135	AGWNGWYS	DMWNH---GQGDPA	-WETFTKELRHLLERD	WGAGSNRYV-----	AGLS	183	
QY	167	MAGSSAMT	LAAYHPQQF	-----	IYAGSLALLDPQSGMGPS	LIGLAMGDAGGY--	KAADMW	220
Db	184	MGGQALY	YAARHPGMFRATAF	SGSAHPLNDES	-----	VDRIMGFFAGQNDPLRW	237	
QY	221	GPSDDPA	-----	WERNDPTQIPKLIVANTR	LYWYCGNGT--	PNELGGAN--	IPAETF	270
Db	238	G---DPA	QGIWQAHDPFLAKRL	-RSIPVILSCGD	TGTGTPDPCATS	SALEADFNQR	292	
QY	271	NFVRSSNL	KFODAYNAAGGHNAVF	PNPFGTHSWEYGAQ	LNAMKGD	LOSSLGAG	325	
Db	293	NHALAAELK	-----	RVGARHWTTTFYGGTG	HWAYRELRHAS	IPMLLGLRVG	341	

RESULT	25	
Q9RSJ7		
ID	Q9RSJ7	PRELIMINARY; PRT; 39 AA.
AC	Q9RSJ7:	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE	Antigen 85A (Fragment).	
OS	Mycobacterium tuberculosis.	
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
OX	NCBI_TaxID=1773;	
RN	[1]	

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RP SEQUENCE.
RX MEDLINE=92366936; PubMed=1502498;
RA Wiker H.G., Nagai S., Harboe M., Ljungqvist L.;
RT "A family of cross-reacting proteins secreted by Mycobacterium tuberculosis.";
RL Scand. J. Immunol. 36:307-319(1992).
DR HSP; P31953; 1DQY..
DR InterPro; IPR00801; Esterase_put.
DR Pfam; PF00756; Esterase; 1.
SQ SEQUENCE 39 AA; 4221 MW; 6E7684361E1B844 CRC64;

Query Match 11.0%; Score 192; DB 2; Length 39;
Best Local Similarity 94.9%; Pred. No. 6.5e-08;
Matches 37; Conservative 1; Mismatches 1; Indels 0; Gaps

Qy 41 FSRPGLPVEYLQVPSMGRDIKVQFQSGGNNSPAYLL 79
|||||
Db 1 FSRPGLPVEYLQVPSMGRDIKVQFQSGGNSPALYLL 39

RESULT 26
Q93JZ6 PRELIMINARY; PRT; 50 AA.
ID Q93JZ6
IC Q93JZ6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ag85A (Fragment).
DN FBPA.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
[.]
RN SEQUENCE FROM N.A.
RC STRAIN=DO69;
RC Maria G.J.;
RN Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

```

Menendez C.;
"Characterization of a M. intracellulare variant strain by molecular techniques.";
Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AJ306712; CACS1392.1; -.
Interpro: IPR00801; Esterase_put.
Pfam: PF00756; Esterase. 1.
NON TER 1 1
NON TER 50 50
SEQUENCE 50 AA: 5170 MW: 6B6071C613B364576 CRC64;

	Query Match	9.6%	Score 167;	DB 2;	Length 50;
Best Local Similarity	66.7%;	Pred. No. 7.28-06;			
Matches	32; Conservative	7; Mismatches	9; Indels	0; Gaps	
QY	169	GSSAMILAAVHPQOFIVAGSLISALLDPSSQGMPSLIGLIGAMDAGGYKA	216		
th	1	GCSSALLIATVYPOOPFPYAAALSGFINSEGWPPPTLIGLAMSIDSQGYKA	48		

RESULT 27

Q99ZY1	
ID	Q99ZY1
AC	PRELIMINARY; PRT; 261 AA.
DT	Q99ZY1, 01-JUN-2001 (TReMBLrel. 17, Created)
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	Pucatec tributyrin esterase.
GN	ESTA OR SPY1022.
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.

OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.

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OX NCBI_TaxID=1314;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
DR EMBL: AB006547; AA033917.1; -
DR InterPro: IPR000801; Esterase_put.
DR InterPro: IPR000379; Ser_estr_site.
DR Pfam: PF00756; Esterase; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30033 MW; D68C339DBB6580D CRC64;

Query Match 9.6%; Score 167; DB 16; Length 261;
Best Local Similarity 25.1%; Pred. No. 6.5e-05;
Matches 73; Conservative 39; Mismatches 109; Indels 70; Gaps 15;

QY 46 LPVEYLQVPSMGRDIKQVF-----QSGGNNSPAVYLLDGLRAODDNGWDINTP 96
Db 4 IAEIHSVVL-GMERKVNVIYDQSEIPKQDQKDIPIVYLLHGMGNE--NSWQKRTA 60
QY 97 AFEWYQSGLSIVMPVGGQSFYSWSPACGKAGCQTYKWTFTLSELQWLISA---NR 153
Db 61 IERLLRHNLIVMP-----STDLGWYTDTA--YGLNYR---ALSQELPQVLAAPFPNM 110
QY 154 AVKPTGSAAGLSMAGSSAMILAAHYHPOQFIYAGLSALLDPSQGMGPSLIGLAMDAGG 213
Db 111 TQKREKTFVAGLSMGYGA-FKWLKSNRFSVAASFSGALDFSP---ETLLEGNLGEAY 166
QY 214 YKAADMWGPSSDPAPERNDPTQIQPKLVANN---TRLWYCGNGTPELGGANIPAEFLE 270
Db 167 WQG--VFQGFDDPLDKH---YLKNMVAESDGKTKFYAWCG-----YE 204
QY 271 NFVRSSNLKFQDAYNAAG-----GHNAVFNPNGTHSWYWGQALNAM 314
Db 205 DFLFATNEKATADFAQGLDIDYHKGH-----GKHEWYWNQQLLEVL 246

RESULT 28
Q8P189 PRELIMINARY; PRT; 261 AA.
AC Q8P189;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Putative tributyrin esterase.
GN ESTA OR SPYM18.1005 OR SPYM3.0658.
OS Streptococcus pyogenes (serotype M18), and
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103, 198466;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR [2]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;

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RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).
DR EMBL: AE010028; AAL97642.1; -
DR EMBL: AE014150; AAM79265.1; -
DR InterPro: IPR000801; Esterase_put.
DR InterPro: IPR000379; Ser_estr_site.
DR Pfam: PF00756; Esterase; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 261 AA; 30019 MW; D2DD768DFA628E7A CRC64;

Query Match 9.5%; Score 166; DB 16; Length 261;
Best Local Similarity 25.1%; Pred. No. 7.7e-05;
Matches 73; Conservative 39; Mismatches 109; Indels 70; Gaps 15;

QY 46 LPVEYLQVPSMGRDIKQVF-----QSGGNNSPAVYLLDGLRAODDNGWDINTP 96
Db 4 IAEIHSVVL-GMERKVNVIYDQSEIPKQDQKDIPIVYLLHGMGNE--NSWQKRTA 60
QY 97 AFEWYQSGLSIVMPVGGQSFYSWSPACGKAGCQTYKWTFTLSELQWLISA---NR 153
Db 61 IERLLRHNLIVMP-----STDLGWYTDTA--YGLNYR---ALSQELPQVLAAPFPNM 110
QY 154 AVKPTGSAAGLSMAGSSAMILAAHYHPOQFIYAGLSALLDPSQGMGPSLIGLAMDAGG 213
Db 111 TQKREKTFVAGLSMGYGA-FKWLKSNRFSVAASFSGALDFSP---ETLLEGNLGEAY 166
QY 214 YKAADMWGPSSDPAPERNDPTQIQPKLVANN---TRLWYCGNGTPELGGANIPAEFLE 270
Db 167 WQG--VFQGFDDPLDKH---YLKNMVAESDGKTKFYAWCG-----YE 204
QY 271 NFVRSSNLKFQDAYNAAG-----GHNAVFNPNGTHSWYWGQALNAM 314
Db 205 DFLFATNEKATADFAQGLDIDYHKGH-----GKHEWYWNQQLLEVL 246

RESULT 29
Q9R505 PRELIMINARY; PRT; 37 AA.
AC Q9R505;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Antigen 85C (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE.
RX MEDLINE=92366936; PubMed=1502498;
RA Wiker H.G., Nagai S., Harboe M., Ljungqvist L.;
RT "A family of cross-reacting proteins secreted by Mycobacterium
RT tuberculosis.";
RL Scand. J. Immunol. 36:307-319 (1992).
DR HSSP: P31953; 1DQV.
DR InterPro: IPR000801; Esterase_put.
DR Pfam: PF00756; Esterase; 1.
SQ SEQUENCE 37 AA; 4016 MW; 08574C9E503DD953 CRC64;

Query Match 8.9%; Score 156; DB 2; Length 37;
Best Local Similarity 84.6%; Pred. No. 3.3e-05;
Matches 33; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 41 FSRPGLPVEYLQVPSMGRDIKQVFQSGGNNSPAVYLL 79
Db 1 FSRPGLPVEYLQVPSMGRDIKQVFQGGPH--AVYLL 37

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Fri Feb 6 13:54:48 2004

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RESULT 30
Q8VKB0 PRELIMINARY; PRT; 94 AA.
ID Q8VKB0
AC Q8VKB0; 201-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein MT0973.
GN MT0973.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE006982; AAK45221.1; -.
DR TIGR; MT0973; -.
KW Hypothetical protein.
SQ SEQUENCE 94 AA; 10869 MW; 32B9F4BA930DED99 CRC64;
Query Match 8.3%; Score 144.5; DB 16; Length 94;
Best Local Similarity 43.2%; Pred. No. 0.00086;
Matches 35; Conservative 3; Mismatches 26; Indels 17; Gaps 3;
QY 246 RLWVYCGNTPN-ELGGANIPAEFLENFVRSSNLKFDAYNAGGHNAVFNPNGTSHW 304
DB 11 RIWVSGNGTPTSAELSGNRRQA-----LQSKYQAA---QRRNFEDGETHW 54
QY 305 EYWGALNNAKGDLSQSLGAG 325
DB 55 AYWRAPLQANLPDLQRLVLDG 75

```

Search completed: February 5, 2004, 17:40:07
Job time : 52.2024 secs

APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-33

Query Match 100.0%; Score 1745; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Qy 61 DIKVOFQSGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFS 120
Db 61 DIKVOFQSGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFS 120
Qy 121 DWYSPACGKAGCQTKWETFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
Db 121 DWYSPACGKAGCQTKWETFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
Qy 181 QOFTYAGLSALLDPSQGMGSLIGLAMDGAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
Db 181 QOFTYAGLSALLDPSQGMGSLIGLAMDGAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
Qy 241 VANNTRLWVYCGNTPNELGGANIPAEFLENFVSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANNTRLWVYCGNTPNELGGANIPAEFLENFVSSNLKFQDAYNAAGGHNAVFNPNG 300
Qy 301 THSWEYGAQLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQLNAMKGDLOSSLGAG 325

RESULT 2
US-08-997-362-33
; Sequence 33, Application US/08997362
; Patent No. 5985287

GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-33

Query Match 100.0%; Score 1745; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Qy 61 DIKVOFQSGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFS 120
Db 61 DIKVOFQSGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFS 120
Qy 121 DWYSPACGKAGCQTKWETFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
Db 121 DWYSPACGKAGCQTKWETFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAVHP 180
Qy 181 QOFTYAGLSALLDPSQGMGSLIGLAMDGAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
Db 181 QOFTYAGLSALLDPSQGMGSLIGLAMDGAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
Qy 241 VANNTRLWVYCGNTPNELGGANIPAEFLENFVSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANNTRLWVYCGNTPNELGGANIPAEFLENFVSSNLKFQDAYNAAGGHNAVFNPNG 300
Qy 301 THSWEYGAQLNAMKGDLOSSLGAG 325

Db 301 THSWEYGAQLNAMKGDLOSSLGAG 325
|||||
RESULT 3
US-08-873-970-33
; Sequence 33, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C1
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-873-970-33
Query Match 100.0%; Score 1745; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSMGR 60
Db 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
QY 121 DWYSPACGKAGCCTYKWEFTLSELQWLANSRPAVKPTGSAATGLSMAGSSAMILAAHP 180
Db 121 DWYSPACGKAGCCTYKWEFTLSELQWLANSRPAVKPTGSAATGLSMAGSSAMILAAHP 180
QY 181 QOFIYAGSLALLDPQSGGNNPSLIGLAWGDAGGYKAADMWGSSDDPAWERNPTQIQPKL 240
Db 181 QOFIYAGSLALLDPQSGGNNPSLIGLAWGDAGGYKAADMWGSSDDPAWERNPTQIQPKL 240

QY 241 VANNTLWVYCGNGTPELGGANI PAEFLFNVRSSNLKFO DAYNAAGGHNAVFPPNG 300
Db 241 VANNTLWVYCGNGTPELGGANI PAEFLFNVRSSNLKFO DAYNAAGGHNAVFPPNG 300
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQLNAMKGDLOSSLGAG 325
RESULT 4
US-09-095-855-33
; Sequence 33, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C3
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-095-855-33
Query Match 100.0%; Score 1745; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSMGR 60
Db 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120

Db 61 DIKVQFSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSPYS 120
QY 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
Db 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
Db 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
QY 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
QY 301 THSWEYGAQNLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQNLNAMKGDLOSSLGAG 325

RESULT 6

US-09-324-542-33
; Sequence 33, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; FILE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-324-542-33

Query Match 100.0%; Score 1745; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVQFSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSPYS 120
Db 61 DIKVQFSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSPYS 120
QY 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
Db 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
Db 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
QY 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
QY 301 THSWEYGAQNLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQNLNAMKGDLOSSLGAG 325

RESULT 7

US-08-690-347-1

QY 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
Db 121 DWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
Db 181 QOFTYAGSLALLDPSQGMGSLIGLAMGAGGYKAADMWGPSSDPDAWERNPTQOIPKL 240
QY 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
Db 241 VANTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNPNG 300
QY 301 THSWEYGAQNLNAMKGDLOSSLGAG 325
Db 301 THSWEYGAQNLNAMKGDLOSSLGAG 325

RESULT 5

US-08-705-347A-33
; Sequence 33, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565
; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-705-347A-33

Query Match 100.0%; Score 1745; DB 3; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVQFSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGQSSPYS 120

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; Sequence 1, Application US/08690347
; Patent No. 6383763
; GENERAL INFORMATION:
; APPLICANT: Wallis, Robert S.
; TITLE OF INVENTION: DETECTION OF MYCOBACTERIA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,347
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: CASE-02270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-690-347-1

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Query Match          100.0%; Score 1745; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWRRIMIGTAAAVVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWRRIMIGTAAAVVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYS 120
QY 121 DWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTGSAAILGLSMAGSSAMILAAVHP 180
Db 121 DWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTGSAAILGLSMAGSSAMILAAVHP 180
QY 181 QQFIYAGSLALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDDPTQIIPKL 240
Db 181 QQFIYAGSLALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDDPTQIIPKL 240
QY 241 VANNTRLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAGGHNANVFPPNG 300
Db 241 VANNTRLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAGGHNANVFPPNG 300
QY 301 THSWYWGALNMGKDLQSSLGAG 325
Db 301 THSWYWGALNMGKDLQSSLGAG 325

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RESULT 8

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US-09-205-426-33
; Sequence 33, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.

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; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-205-426-33

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Query Match          100.0%; Score 1745; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWRRIMIGTAAAVVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWRRIMIGTAAAVVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFYS 120
QY 121 DWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTGSAAILGLSMAGSSAMILAAVHP 180
Db 121 DWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTGSAAILGLSMAGSSAMILAAVHP 180
QY 181 QQFIYAGSLALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDDPTQIIPKL 240
Db 181 QQFIYAGSLALLDPSCQMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDDPTQIIPKL 240
QY 241 VANNTRLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAGGHNANVFPPNG 300
Db 241 VANNTRLWYCGNGTPELGGANI PAEFLNFVRSSNLKFQDAYNAGGHNANVFPPNG 300
QY 301 THSWYWGALNMGKDLQSSLGAG 325
Db 301 THSWYWGALNMGKDLQSSLGAG 325

```

RESULT 9

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US-09-200-643-33
; Sequence 33, Application US/09200643
; Patent No. 6410720
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002CON
; CURRENT APPLICATION NUMBER: US/09/200,643
; EARLIER FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-09-200-643-33

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Fri Feb 6 13:54:46 2004

us-09-805-427a-2.116min.ra1

Query Match 100.0%; Score 1745; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 2.5e-161;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60

QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFY 120
DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFY 120

QY 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
DB 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180

QY 181 QOFTYAGLSALLDPSQGMGSLILGLAMGDAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
DB 181 QOFTYAGLSALLDPSQGMGSLILGLAMGDAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240

QY 241 VANNTRLMVYCGNGTNPNEGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300
DB 241 VANNTRLMVYCGNGTNPNEGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300

QY 301 THSWEYGAQINAMKGDLOSSLGAG 325
DB 301 THSWEYGAQINAMKGDLOSSLGAG 325

RESULT 10
US-08-107-676-29
; Sequence 29, Application US/08107676
; Patent No. 5955356
; GENERAL INFORMATION:
; APPLICANT: Content, Jean
; APPLICANT: DeBruyn, Jacqueline
; TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
; TITLE OF INVENTION: Tuberculosis
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould
; STREET: 3100 No. 5955356west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,676
; FILING DATE: 04-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00268
; FILING DATE: 07-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91400388.4
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 8076.89USWO
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Mycobacterium bovis
IMMEDIATE SOURCE:
CLONE: Antigen 85B protein sequence from
CLONE: alpha-antigen of M.bovis
US-08-107-676-29

Query Match 99.0%; Score 1728; DB 2; Length 325;
Best Local Similarity 99.1%; Pred. No. 1.1e-159;
Matches 322; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60

QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFY 120
DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFY 120

QY 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
DB 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180

QY 181 QOFTYAGLSALLDPSQGMGSLILGLAMGDAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240
DB 181 QOFTYAGLSALLDPSQGMGSLILGLAMGDAGGYKAADMWGPSSDPPOWERNDPTQOIPKL 240

QY 241 VANNTRLMVYCGNGTNPNEGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300
DB 241 VANNTRLMVYCGNGTNPNEGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300

QY 301 THSWEYGAQINAMKGDLOSSLGAG 325
DB 301 THSWEYGAQINAMKGDLOSSLGAG 325

RESULT 11
US-08-997-080-35
; Sequence 35, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-080-35

Query Match 97.8%; Score 1706; DB 2; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60

Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60

QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120

Db 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120

QY 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180

Db 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180

QY 181 QQFIYAGSLALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDDPAWERNPTQQIPKL 240

Db 181 QQFIYAGSLALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDDPAWERNPTQQIPKL 238

QY 241 VANNTRLVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYKAGGNAVFNFPNG 300

Db 239 VANNTRLVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYKAGGNAVFNFPNG 298

QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325

Db 299 THSWEYGAQLNAMKGDLOSSLGAG 323

RESULT 12

US-08-997-362-35

Sequence 35, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/973,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-35

Query Match 97.8%; Score 1706; DB 2; Length 323;

Best Local Similarity 98.5%; Pred. No. 1.5e-157;

Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60

Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGAATAGAFSRPGLPVEYLQVPSMGR 60

QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120

Db 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120

QY 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180

Db 121 DWSPACGKAGCQTYKWTETLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILAAAYHP 180

QY 181 QQFIYAGSLALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDDPAWERNPTQQIPKL 240

Db 181 QQFIYAGSLALLDPSQGMPSLIGLAMGDAGGYKAADMWGPSSDDPAWERNPTQQIPKL 238

QY 241 VANNTRLVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYKAGGNAVFNFPNG 300

Db 239 VANNTRLVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYKAGGNAVFNFPNG 298

QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325

Db 299 THSWEYGAQLNAMKGDLOSSLGAG 323

RESULT 13

US-08-873-970-35

Sequence 35, Application US/08873970

Patent No. 6001361

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

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SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,970
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-873-970-35

Query Match          97.8%; Score 1706; DB 3; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

1 MTDVSRKIRAWGRRLMIGTAAVVLGLVCLAGATAGAFSPGLPEVLYQVPSQWGR 60

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61	QY	DIKVPQSGGNNSPAVYLLDGLRAODDYNQWDINTPAFEWYQSGLSIVMPVGGQSSFS	120
61	Db	DIKVPQSGGNNSPAVYLLDGLRAODDYNQWDINTPAFEWYQSGLSIVMPVGGQSSFS	120
121	QY	DWYSPACGKAGCOTYKWETFTLTSLPWLSANRAVKPTGSAAGLSMAGSSAMTAAAYHP	180
121	Db	DWYSPACGKAGCOTYKWETFTLTSLPWLSANRAVKPTGSAAGLSMAGSSAMTAAAYHP	180
181	QY	QQFIYAGSLSALLDPSQGMGSLTGLAMGAGGYKAADMGPSSDPPOWERNDPTQQIPKL	240
181	Db	QQFIYAGSLSALLDPSQGMG--LIGLAMGAGGYKAADMGPSSDPPOWERNDPTQQIPKL	238
241	QY	VANNTRLWVYCGNTPNELGANTPAEFLNFVRSNLLKFQDAYNAAGHNAVNFPNG	300
239	Db	VANNTRLWVYCGNTPNELGANTPAEFLNFVRSNLLKFQDAYNPAGHNAVNFPNG	298
301	QY	THSWEYGAQLNAMKGDLOSSLGAG	325
299	Db	THSWEYGAQLNAMKGDLOSSLGAG	323

RESULT 14

US-09-095-855-35

; Sequence 35, Application US/09095855

; Patent No. 6160093

; GENERAL INFORMATION:

APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
Treatment and Diagnosis of Mycobacterial Infections
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

```

; TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565
; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 323 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-705-347A-35

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Query Match          97.8%; Score 1706; DB 3; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
QY 121 DWYSPACGKAGCQTYKWETLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAHP 180
DB 121 DWYSPACGKAGCQTYKWETLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAHP 180
QY 181 QQFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNNDPTQQIPKL 240
DB 181 QQFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNNDPTQQIPKL 240
QY 241 VANNTRLWYVCGTGNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFG 300
DB 239 VANNTRLWYVCGTGNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFG 300
QY 301 THSWEYWGQALNMGKDLQSSILGAG 325
DB 299 THSWEYWGQALNMGKDLQSSILGAG 323

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RESULT 16
US-09-324-542-35
; Sequence 35, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS

```

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; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
; US-09-324-542-35

Query Match          97.8%; Score 1706; DB 4; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGVLGAGGAATAGAFSPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
DB 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
QY 121 DWYSPACGKAGCQTYKWETLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAHP 180
DB 121 DWYSPACGKAGCQTYKWETLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAHP 180
QY 181 QQFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNNDPTQQIPKL 240
DB 181 QQFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNNDPTQQIPKL 240
QY 241 VANNTRLWYVCGTGNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFG 300
DB 239 VANNTRLWYVCGTGNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFG 300
QY 301 THSWEYWGQALNMGKDLQSSILGAG 325
DB 299 THSWEYWGQALNMGKDLQSSILGAG 323

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RESULT 17
US-09-205-426-35
; Sequence 35, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; OF MYCOBACTERIAL INFECTIONS
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
; US-09-205-426-35

```

```

Query Match          97.8%; Score 1706; DB 4; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMR 60
QY 61 DIKVQFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYS 120
Db 61 DIKVQFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYS 120
QY 121 DWTSPACGKAGCCTYKWEFTLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHP 180
Db 121 DWTSPACGKAGCCTYKWEFTLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHP 180
QY 181 QQFIYAGSLALLDPSQCMGSLIGLAWDAGGKAAADMWGPSSDDPAWERNPTQOIPKL 240
Db 181 QQFIYAGSLALLDPSQCMG--LIGLAWDAGGKAAADMWGPSSDDPAWERNPTQOIPKL 238
QY 241 VANNTRLVVYCGNGTNPNEGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVENFPFNG 300
Db 239 VANNTRLVVYCGNGTNPNEGANIPAEFLENFVRSSNLKFODAYKPAGGHNAVENFPFNG 298
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
Db 299 THSWEYGAQLNAMKGDLOSSLGAG 323
RESULT 18
US-09-200-643-35
; Sequence 35, Application US/09200643
; Patent No. 6410720
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002CON
; CURRENT APPLICATION NUMBER: US/09/200,643
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-09-200-643-35
Query Match 97.8%; Score 1706; DB 4; Length 323;
Best Local Similarity 98.5%; Pred. No. 1.5e-157; Indels 2; Gaps 1;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMR 60
QY 61 DIKVQFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYS 120
Db 61 DIKVQFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYS 120
QY 121 DWTSPACGKAGCCTYKWEFTLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHP 180
Db 121 DWTSPACGKAGCCTYKWEFTLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHP 180
QY 181 QQFIYAGSLALLDPSQCMGSLIGLAWDAGGKAAADMWGPSSDDPAWERNPTQOIPKL 240
Db 181 QQFIYAGSLALLDPSQCMG--LIGLAWDAGGKAAADMWGPSSDDPAWERNPTQOIPKL 238
QY 241 VANNTRLVVYCGNGTNPNEGANIPAEFLENFVRSSNLKFODAYNAAGGHNAVENFPFNG 300
Db 239 VANNTRLVVYCGNGTNPNEGANIPAEFLENFVRSSNLKFODAYKPAGGHNAVENFPFNG 298
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325

Db 299 THSWEYGAQLNAMKGDLOSSLGAG 323
RESULT 19
US-08-508-761B-33
; Sequence 33, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Armel
; APPLICANT: Purification, Relano
; APPLICANT: Duchiron, Francis
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; TITLE OF INVENTION: Secretion Especially in Corynebacteria
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: M. bovis
US-08-508-761B-33
Query Match 93.0%; Score 1623; DB 3; Length 307;
Best Local Similarity 98.4%; Pred. No. 1.6e-149;
Matches 304; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 17 IGTAATAVPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMRDIKVQFQSGGNNSPAV 76
Db 1 IGTAATAVPLGLVGLAGGAATAGAFSRPGLPVEYLQVPSFSGMRDIKVQFQSGGNNSPAV 60
QY 77 YLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYSWYSPACGKAGCCTYK 136
Db 61 YLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFYSWYSPACGKAGCCTYK 120
QY 137 WETFLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHPQQFIYAGSLALLDPS 196
Db 121 WETFLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAAYHPQQFIYAGSLALLDPS 180
QY 197 QMGPSLIGLAWDAGGKAAADMWGPSSDDPAWERNPTQOIPKL VANNTRLVVYCGNGT 256

Db 181 QCMG--LIGLAMDAGGYKAAADWGFSSDPARNDPTQIQIPKLVANNTRLVYCGNGTF 238
QY 257 NELGANTPABLFENFVRSSNLKFDADYNAAGHNAVFNPNGTHSWEYGAQINAMKG 316
Db 239 NELGANTPABLFENFVRSSNLKFDADYNAAGHNAVFNPNGTHSWEYGAQINAMKG 298
QY 317 DQSSLGAG 325
Db 299 DQSSLGAG 307

RESULT 20
US-09-051-755-16
; Sequence 16, Application US/09051755
; Patent No. 6506389
; GENERAL INFORMATION:
; APPLICANT: LEER, Robert J
; APPLICANT: FOUWELS, Pieter H
; APPLICANT: CONWAY, Patricia L
; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND FOOD ADDITIVES C
; FILE REFERENCE: LEER et al. 09/051.755
; CURRENT APPLICATION NUMBER: US/09/051.755
; EARLIER FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: PCT/NL95/00367
; EARLIER FILING DATE: 1995-10-20
; EARLIER APPLICATION NUMBER: PCT/NL96/00409
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: aligned aa
; OTHER INFORMATION: sequence of Mycobacterium Mtu85b
; NAME/KEY: UNSURE
; LOCATION: (1)..(364)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-051-755-16

Query Match 92.4%; Score 1612; DB 4; Length 364;
Best Local Similarity 92.6%; Pred. No. 2.4e-148;
Matches 325; Conservative 0; Mismatches 0; Indels 26; Gaps 12;

QY 1 MTDVSRKIRA---WGRRLMIGTAAAVLPLGLVGLAGGATAGAFSRPG-LPVEYLQVPS 55
Db 3 MTDVSRKIRAXXXXWGRRLMIGTAAAVLPLGLVGLAGGATAGAFSRPG-LPVEYLQVPS 62
QY 56 P-SMGDRDKV-QFQSGGNSPAVYLLDGLRAQDDY--NGWDINTPAFEWYQSG-LSIYV 110
Db 63 PSMGDRDKVQFQSGGNSPAVYLLDGLRAQDDYXXNGWDINTPAFEWYQSGXLSIYV 122
QY 111 PVGGQSSFYSDWYSPACGACGCTYKWT-FLTSELPOWLSANRAVKPTGSAAGI----- 165
Db 123 PVGGQSSFYSDWYSPACGACGCTYKWTXFLTSELPOWLSANRAVKPTGSAAGI----- 182
QY 166 --SMAGSS---AMLAAYHPQOFI---YAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 217
Db 183 XASMAGSSXXXAMLAAYHPQOFIXXXYAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 242
QY 218 DMWGSSDDPAWRNDPTQIQIPKLVANNTRLVYCGNGTNEELGGANI PAEFLFNFRSSN 277
Db 243 DMWGSSDDPAWRNDPTQIQIPKLVANNTRLVYCGNGTNEELGGANI PAEFLFNFRSSN 302
QY 278 LKFDAYNAAGHNAVFNPNGTHSWE--YGAQINAMKGLQSSSL--GAG 325
Db 303 LKFDAYNAAGHNAVFNPNGTHSWEYXXYGAQINAMKGLQSSSLXGAG 353

RESULT 21
US-08-107-676-30
; Sequence 30, Application US/08107676
; Patent No. 5955356
; GENERAL INFORMATION:
; APPLICANT: Content, Jean
; APPLICANT: DeWit, Lucas
; APPLICANT: DeBruyn, Jacqueline
; TITLE OF INVENTION: Mycobacterium Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding Them for Diagnosis and Control of
; TITLE OF INVENTION: Tuberculosis
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5955356west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/107,676
; FILING DATE: 04-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00268
; FILING DATE: 07-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91400388.4
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 8076.89USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium kansasii
; IMMEDIATE SOURCE:
; CLONE: Partial protein sequence from antigen 85B
; CLONE: from M.kansasii
US-08-107-676-30

Query Match 92.2%; Score 1609; DB 2; Length 325;
Best Local Similarity 89.8%; Pred. No. 4e-148;
Matches 291; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVGLAGGATAGAFSRPG-LPVEYLQVPSMGR 60
Db 1 MTDVSGKIRAWGRRLLVGAATAALPLGLVGLAGGATAGAFSRPG-LPVEYLQVPSAAMGR 60
QY 61 DIKVOFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIYMPVGGQSSFY 120
Db 61 SIKVOFQSGGNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIYMPVGGQSSFY 120
QY 121 DWYSPACGACGCTYKWTFLTSELPOWLSANRAVKPTGSAAGI-SMAGSSAMLAAYHP 180
Db 121 DWYSPACGACGCTYKWTFLTSELPOWLSANRAVKPTGSAAGI-SMAGSSAMLAAYHP 180
QY 181 QOFTYAGSLSALLDPSQGMGPSLIGLAMDAGGYKAAADWGFSSDPARNDPTQIQIPKL 240

```

Db 181 QQFIYAGSLALMDPSQGMGPSLIGLAMGDAGGYKASDMWGPSSDPAWQRNDPSLHPEL 240
QY 241 VANNTRLWYCGTGNELGANIPAEFFLENFVRSSNLKFDQDAYNAAGGNVNFPPNG 300
Db 241 VANNTRLWYCGTGNELGANIPAEFFLENFVRSSNLKFDQDAYNAAGGNVNFPPNG 300
QY 301 THSWEYGAQLNAMKGLQSSIGA 324
Db 301 THSWEYGAQLNAMKGLQSSIGA 324

RESULT 22
US-08-508-761B-32
; Sequence 32, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Arnel
; APPLICANT: Duchiron, Relano
; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; SECRETION Especially in Corynebacteria
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: M. kansaii
US-08-508-761B-32

Query Match 88.0%; Score 1536; DB 3; Length 309;
Best Local Similarity 89.9%; Pred. No. 4.6e-141;
Matches 277; Conservative 19; Mismatches 12; Indels 0; Gaps 0;

QY 17 ICTAAAVLPGVLGAGGATAGAFSRPGLPVEYLVQVPSMGDR:KVQFQSGGNSPAV 76
Db 1 VAAAAAALPGVLGAGGATAGAFSRPGLPVEYLVQVPSMGDR:KVQFQSGGNSPAV 60
QY 77 YLDDGLRAQDYGNDINTPAFEWYQSLIVMPVGGQSSFYSDWYSPACGKAGCOTYK 136
Db 61 YLDDGLRAQDYGNDINTPAFEWYQSLIVMPVGGQSSFYSDWYSPACGKAGCOTYK 120

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QY 137 WETFLTSELQWL SANRAVKPTGSAALGLSMAGSSAMILAAHYHPQQFIYAGSLALDPS 196
Db 121 WETFLTSELQWL SANRAVKPTGSAALGLSMAGSSAMILAAHYHPQQFIYAGSLALDPS 180
QY 197 QGMGPSLIGLAMGDAGGYKASDMWGPSSDPAWQRNDPSLHPEL VANNTRLWYCGNGTP 256
Db 181 QGMGPSLIGLAMGDAGGYKASDMWGPSSDPAWQRNDPSLHPEL VANNTRLWYCGNGTP 240
QY 257 NELGGANIPAEFFLENFVRSSNLKFDQDAYNAAGGNVNFPPNGTHSWEYGAQLNAMKG 316
Db 241 SELGGANVPAEFFLENFVRSSNLKFDQDAYNAAGGNVNFNDANGTHSWEYGAQLNAMKG 300
QY 317 DLOSSLGA 324
Db 301 DLOSSLGA 308

RESULT 23
US-08-690-347-2
; Sequence 2, Application US/08690347
; Patent No. 6383763
; GENERAL INFORMATION:
; APPLICANT: Wallis, Robert S.
; TITLE OF INVENTION: DETECTION OF MYCOBACTERIA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,347
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: CASE-02270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-690-347-2

Query Match 87.2%; Score 1522; DB 4; Length 330;
Best Local Similarity 84.9%; Pred. No. 1.1e-139;
Matches 275; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGVLGAGGATAGAFSRPGLPVEYLVQVPSMGDR 60
Db 1 MTDLSKVRAGRRLVAGAAAVLPGVLGAGGATAGAFSRPGLPVEYLVQVPSMGDR 60
QY 61 DIKVQFQSGGNSPAVYLLDGLRAQDYGNDINTPAFEWYQSLIVMPVGGQSSFY 120
Db 61 DIKVQFQSGGNSPAVYLLDGLRAQDYGNDINTPAFEWYQSLIVMPVGGQSSFY 120
QY 121 DWYSPACGKAGCOTYKWTFLTSELQWL SANRAVKPTGSAALGLSMAGSSAMILAAHYHP 180
Db 121 DWYSPACGKAGCOTYKWTFLTSELQWL SANRAVKPTGSAALGLSMAGSSAMILAAHYHP 180

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Qy	181	QQFYAGSLSDLPSCMGPSFLTGLANGDAGGYKADAWGSPSSDPAMERNDP	QOI PKL 240
Dd	181	DQFYAGSLSDLPSCMGPSFLTGLANGDAGGYKADAWGSPSSDPAMQRNDS	LHI PBL 240
Qy	241	VANTRILWYCGNGTPNELGGANTPAEFLNFVRSSNTLKFDAYNAAGGHNAVFP	PNG 300
Dd	241	VGNTRILWYCGNGTPSELGANMPAEFLNFVRSSNLKFQDAYNGAGGHNAVFN	ANG 300
Qy	301	THSWEYGAQLNAMKGDLQSSIGA	324
Dd	301	THSWEYGAQLNAMKPDLQGTIGA	324

RESULT 24

US-08-311-731A-83
Sequence 83, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-83

Query Match 83.4%; Score 1455; DB 4; Length 327;
Best Local Similarity 83.0%; Pred. No. 3.6e-133;
Matches 269; Conservative 19; Mismatches 34; Indels

1 MTDVSRKIRAWGRRLMIGTAAAVLPLGLVLGAGGAATAGAFSPGLPVEYLQVPSPMGR 60
 |||||
 1 MIDVSGKIRAWGRLLVG--AAATPLSLISLAGGAATASAFSPGLPVEYLQVPSPMGR 58
 |||||
 61 DIKVFQSGGNGSPAVLLDGLRAQDDYNGWDINTAFEFWYQSGLSIYMPVGGQSSFFS 120
 |||||
 59 SIKVFQNGGNGSPAVLLDGLRAQDDYNGWDINTSAFEWYQSGLSVYMPVGGQSSFFS 118
 |||||
 121 DWYSPAGKAGCQYKNEFTLTSELPOWLSANRAVKTPTSAATGLSMAGSSAMILAAVHP 180
 |||||

Db	119	DWSPACGKAGCTTYKWTETLTSELPKWL SANRSVKSTGSAVVGLSMAGSSALILAAVHP	178
Qy	181	QQFIYAGSLGALLDPSOGMGPSSILGLAMGDAGGYKAADMMGPPSDPAWERNDPTQCIPEKL	240
Db	179	DQFIYAGSLGALLDPSOGIPEQLIGLAMGDAGGYKAADMMGPPNDPAWQRNDPTLQAGKL	238
Qy	241	VANNRLWVYCGNGTNPNEGGANIPAEFLFNFRSSNLKFODAYNAAGCHNAVFNPFPNG	300
Db	239	VANNTHLWVYCGNGTPELSELTGTVPAEFLFNFRVHGSNLKFQDAYNGAGGCHNAVFNLNADG	298
Qy	301	THSWEYWGAGQINAMKGDLOSSLGA	324
Db	299	THSWEYWGAGQINAMKPDLONTLMA	322

RESULT 25

US-08-997-080-31
Sequence 31, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-31

Query Match	Score 1454	DB 2	Length 327
Best Local Similarity	83.3%	Score 1454	DB 2
Best Local Similarity	83.3%	Score 1454	DB 2

	Matches	269;	Conservative	19;	Mismatches	34;	Indels	2;	Gaps	1;
QY	1	MTDVS	KIRAWGRRL	MIGTAAAV	PGLVGLAGGA	TATAGAR	PRGLPEYLQVPS	MGR	60	
Db	1	MIDVSG	KIRAWGRW	LIVG--AAAT	PLSLSLAGGA	TATAGAR	PRGLPEYLQVPS	MGR	58	
QY	61	DIKVQF	QSGGNNSP	AVYLLDGL	RAQDDYNG	WDINTAF	EYFYQSLGSLVMP	VGQSS	120	
Db	59	TIKVQF	QGGNGSP	AVYLLDGL	RAQDDYNG	WDINTAF	EYFYQSLGSLVMP	VGQSS	118	
QY	121	DWTS	PACGKAGCQ	TYKWTFL	TSELPQWL	SANRAV	KPTGSAAGLS	SMAGSSAMIIAAV	HP	180

```

Db 119 DWTSPACGKAGCTTYKWTETLTSELPAKLSANRSVKSTGSAVVGSLMAGSSALILAAHP 178
QY 181 QQFIYAGSLALDPSQGMGSLIGLWAGDAGGYKAAADMMGSPSSDPAWERNDDPTQIPKL 240
Db 179 DQFIYAGSLALDSSQGIPEQLIGLWAGDAGGYKAAADMMGPPNDPAWQNRNDPTLQAGKL 238
QY 241 VANNTRLWVYCGNGTPELGNANIPAEFLENFVRSNNLKFQDAYNAAGGHNAVENFPNG 300
Db 239 VANNTHLWVYCGNGTPELGGTNVPAEFLENFVHGSNLKTFQDAYNGAGGHNAVENLNADG 298
QY 301 THSWEYGAQLNAMKGDLOSSLGA 324
Db 299 THSWEYGAQLNAMKPDQLNTLMA 322

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RESULT 26
US-08-997-362-31
; Sequence 31, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,362
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-362-31

```

```

Query Match 83.3%; Score 1454; DB 2; Length 327;
Best Local Similarity 83.0%; Pred. No. 4.5e-133;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;
QY 1 MTDVSKIRAWGRRLMIGTAAAVLPLGLVLAGGAATAGAFSRPGLFVEYLQVPSPMGR 60

```

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Db 1 MIDVSKIRAWGRLLVG--AAATLPSLISLAGGAATASAFSRPGLFVEYLQVPSEAMGR 58
QY 61 DIKVFQSGGNNPAAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSFFYS 120
Db 59 TIKVFQFQNGSPAAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSFFYS 118
QY 121 DWTSPACGKAGCTTYKWTETLTSELPAKLSANRAVKPTGSAALGSLMAGSSAMILAAHP 180
Db 119 DWTSPACGKAGCTTYKWTETLTSELPAKLSANRSVKSTGSAVVGSLMAGSSALILAAHP 178
QY 181 QQFIYAGSLALDPSQGMGSLIGLWAGDAGGYKAAADMMGSPSSDPAWERNDDPTQIPKL 240
Db 179 DQFIYAGSLALDSSQGIPEQLIGLWAGDAGGYKAAADMMGPPNDPAWQNRNDPTLQAGKL 238
QY 241 VANNTRLWVYCGNGTPELGNANIPAEFLENFVRSNNLKFQDAYNAAGGHNAVENFPNG 300
Db 239 VANNTHLWVYCGNGTPELGGTNVPAEFLENFVHGSNLKTFQDAYNGAGGHNAVENLNADG 298
QY 301 THSWEYGAQLNAMKGDLOSSLGA 324
Db 299 THSWEYGAQLNAMKPDQLNTLMA 322

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RESULT 27
US-08-873-970-31
; Sequence 31, Application US/08873970
; Patent No. 6001361
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,970
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-873-970-31

```

Query Match 83.3%; Score 1454; DB 3; Length 327;
Best Local Similarity 83.0%; Pred. No. 4.5e-133;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;
QY 1 MTDVSKIRAWGRRLMIGTAAAVLVPLGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60
Db 1 MIDVSKIRAWGRWLVG--AAATLPSLISLAGAATASAFSPGLPVEYLQVPSMGR 58
QY 61 DIKVFQSGGNNSPAYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 59 TIKVFQNGGNSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSSFFS 118
QY 121 DWYSPACGKAGCTTYKWTFTLSELQWLSANRAVPTGSAALGLSMAGSSAMILAAHP 180
Db 119 DWYSPACGKAGCTTYKWTFTLSELQWLSANRAVPTGSAALGLSMAGSSAMILAAHP 178
QY 181 QOFIYAGSLALDPSQGMGPSLIGLAMDAGGYKAAAMWGPSSDPAWERNDPTQIPLK 240
Db 179 DQFIYAGSLALDPSQGMGPSLIGLAMDAGGYKAAAMWGPSSDPAWERNDPTQIPLK 238
QY 241 VANNTLWVYCGNGTNPNEGANNIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNPFPNG 300
Db 239 VANNTLWVYCGNGTNPNEGANNIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNLNADG 298
QY 301 THSWEYWGALNMAKGDLOSLGA 324
Db 299 THSWEYWGALNMAKPDQLNTLMA 322
RESULT 28
US-09-805-855-31
; Sequence 31, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-805-855-31

Query Match 83.3%; Score 1454; DB 3; Length 327;
Best Local Similarity 83.0%; Pred. No. 4.5e-133;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;
QY 1 MTDVSKIRAWGRRLMIGTAAAVLVPLGLVGLAGGAATAGAFSPGLPVEYLQVPSMGR 60
Db 1 MIDVSKIRAWGRWLVG--AAATLPSLISLAGAATASAFSPGLPVEYLQVPSMGR 58
QY 61 DIKVFQSGGNNSPAYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFFS 120
Db 59 TIKVFQNGGNSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSSFFS 118
QY 121 DWYSPACGKAGCTTYKWTFTLSELQWLSANRAVPTGSAALGLSMAGSSAMILAAHP 180
Db 119 DWYSPACGKAGCTTYKWTFTLSELQWLSANRAVPTGSAALGLSMAGSSAMILAAHP 178
QY 181 QOFIYAGSLALDPSQGMGPSLIGLAMDAGGYKAAAMWGPSSDPAWERNDPTQIPLK 240
Db 179 DQFIYAGSLALDPSQGMGPSLIGLAMDAGGYKAAAMWGPSSDPAWERNDPTQIPLK 238
QY 241 VANNTLWVYCGNGTNPNEGANNIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNPFPNG 300
Db 239 VANNTLWVYCGNGTNPNEGANNIPAEFLENFVRSSNLKFQDAYNAGGHNAVFNLNADG 298
QY 301 THSWEYWGALNMAKGDLOSLGA 324
Db 299 THSWEYWGALNMAKPDQLNTLMA 322

RESULT 29
US-08-705-347A-31
; Sequence 31, Application US/08705347A
; Patent No. 6284255
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyma, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Speckman Picard PLLC
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,347A
; FILING DATE: 28-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206.269.0565

; TELEFAX: 206.269.0563
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-705-347A-31

Query Match 83.3%; Score 1454; DB 3; Length 327;
Best Local Similarity 83.0%; Pred. No. 4.5e-133;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY	1	MTDVSRIKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR	60
Db	1	MIDVSGKIRAWGRLLVG--AAATPLSLIAGGAATASAFSRPGLPVEYLQVPSMGR	58
QY	61	DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS	120
Db	59	TIKVFQFQNGGSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSSFYS	118
QY	121	DWYSPACGKAGCTTYKWETELTSELPOWLSANRAVKPTGSAALIGLSMAGSSAMILAAHP	180
Db	119	DWYSPACGKAGCTTYKWETELTSELPKWLSANRSVKSTGSAVVGSLMAGSSALILAAHP	178
QY	181	QOFIYAGSLALDPSQGMGPSLIGLAWGDAGGYKAAADMWGPSSDPAWERNDPQQIPKL	240
Db	179	DQFIYAGSLALMDSSQGIPEQLIGLAWGDAGGYKAAADMWGPSSDPAWQRNDPILQAGKL	238
QY	241	VANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVENFPNG	300
Db	239	VANNTHLWVYCGNGTPELGGTNNVPAEFLENFVHGSNLKFQDAYNGAGGHNAVENLNADG	298
QY	301	THSWEYWGALNNAKMDLQSSLGA	324
Db	299	THSWEYWGALNNAKMDLQNTLMA	322

RESULT 30

US-09-324-542-31
; Sequence 31, Application US/09324542
; Patent No. 6328978

GENERAL INFORMATION:

; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: PrestiGge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mycobacterium leprae

US-09-324-542-31

Query Match 83.3%; Score 1454; DB 4; Length 327;
Best Local Similarity 83.0%; Pred. No. 4.5e-133;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY	1	MTDVSRIKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR	60
Db	1	MIDVSGKIRAWGRLLVG--AAATPLSLIAGGAATASAFSRPGLPVEYLQVPSMGR	58
QY	61	DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS	120
Db	59	TIKVFQFQNGGSPAVYLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGQSSFYS	118

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      February 5, 2004, 17:38:58 ; Search time 44.881 Seconds
              (without alignments)
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Title:      US-09-805-427A-2
Perfect score: 1745
Sequence:    1 MTDVSRKIRAGRRRLMIGTA.....YWGQQLNAMKGDQLQSSLGAG 325

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:     801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 788294

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 90 summaries

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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1745	100.0	325	10	US-09-805-427A-2		Sequence 2, Appli
2	1745	100.0	325	11	US-09-880-505-33		Sequence 33, Appl
3	1745	100.0	325	11	US-09-952-554-1		Sequence 1, Appli
4	1745	100.0	325	12	US-09-872-505-2		Sequence 2, Appli
5	1745	100.0	325	14	US-10-051-643-33		Sequence 33, Appl
6	1706	97.8	323	11	US-09-880-505-35		Sequence 35, Appl
7	1706	97.8	323	14	US-10-051-643-35		Sequence 35, Appl
8	1612	92.4	364	9	US-09-051-755-16		Sequence 16, Appl
9	1568.5	82.9	364	15	US-10-231-055-16		Sequence 16, Appl
10	1568.5	89.4	1016	12	US-10-369-983-18		Sequence 18, Appl
11	1557	88.2	1010	9	US-10-369-983-4		Sequence 4, Appli
12	1550	89.8	403	9	US-09-791-171-173		Sequence 173, App
13	1550	88.8	403	10	US-09-805-427A-4		Sequence 4, Appli
14	1550	88.8	403	12	US-09-804-580-173		Sequence 173, App
15	1550	88.8	403	12	US-09-872-505-4		Sequence 4, Appli

[illegible]

89 106.5 6.1 781 15 US-10-156-761-12689 Sequence 12689, A
90 105 6.0 20 10 US-09-813-333-65 Sequence 65, Appl

ALIGNMENTS

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RESULT 1
US-09-805-427A-2
; Sequence 2, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(40)
US-09-805-427A-2

Query Match      100.0%; Score 1745; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 6.1e-157;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
DB 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
QY 121 DWSPACGKAGCQTKWETFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
DB 121 DWSPACGKAGCQTKWETFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QOFTYAGSLALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAPERNDPTQOI PKL 240
DB 181 QOFTYAGSLALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAPERNDPTQOI PKL 240
QY 241 VANNTLRLVYCGNGTPNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFPNG 300
DB 241 VANNTLRLVYCGNGTPNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFPNG 300
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
DB 301 THSWEYGAQLNAMKGDLOSSLGAG 325

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RESULT 2
US-09-880-505-33
; Sequence 33, Application US/09880505
; Publication No. US2003000796A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; FILE REFERENCE: 11000.100722
; CURRENT APPLICATION NUMBER: US/09/880,505
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080

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; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-880-505-33

Query Match      100.0%; Score 1745; DB 11; Length 325;
Best Local Similarity 100.0%; Pred. No. 6.1e-157;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
DB 1 MTDVSRKIRAWGRRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
DB 61 DIKVFQSGGNNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFFYS 120
QY 121 DWSPACGKAGCQTKWETFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
DB 121 DWSPACGKAGCQTKWETFLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180
QY 181 QOFTYAGSLALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAPERNDPTQOI PKL 240
DB 181 QOFTYAGSLALLDPSQGMGPSLIGLAMDAGGYKAADMWGPSSDPAPERNDPTQOI PKL 240
QY 241 VANNTLRLVYCGNGTPNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFPNG 300
DB 241 VANNTLRLVYCGNGTPNELGGANIPAEFLENFVRSSNLKFDQAYNAAGHNAVFNPFPNG 300
QY 301 THSWEYGAQLNAMKGDLOSSLGAG 325
DB 301 THSWEYGAQLNAMKGDLOSSLGAG 325

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RESULT 3
US-09-952-554-1
; Sequence 1, Application US/09952554
; Publication No. US20030036104A1
; GENERAL INFORMATION:
; APPLICANT: Wallis, Robert S.
; TITLE OF INVENTION: DETECTION OF MYCOBACTERIA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,554
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,347
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: CASE-02270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 325 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: No. US20030036104A1 Relevant
;   TOPOLOGY: No. US20030036104A1 Relevant
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-952-554-1

Query Match      100.0%; Score 1745; DB 11; Length 325;
Best Local Similarity 100.0%; Pred. No. 6.1e-157;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSPSMGR 60
QY 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS 120
DB 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS 120
QY 121 DWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKTGSAALGLSMAGSSAMILAAAYHP 180
DB 121 DWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKTGSAALGLSMAGSSAMILAAAYHP 180
QY 181 QOFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
DB 181 QOFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
QY 241 VANNTRLWYCGNGTNPNEGNIIPAEFLNFVRSSNLKFQDAYNAAGHNAVFNPPNG 300
DB 241 VANNTRLWYCGNGTNPNEGNIIPAEFLNFVRSSNLKFQDAYNAAGHNAVFNPPNG 300
QY 301 THSWEYWGQAQLNAMKGDLOSSLGAG 325
DB 301 THSWEYWGQAQLNAMKGDLOSSLGAG 325

RESULT 5
US-10-051-643-33
; Sequence 33, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vacciae
; FILE REFERENCE: 11000.1008C2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-051-643-33

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Query Match      100.0%; Score 1745; DB 14; Length 325;
Best Local Similarity 100.0%; Pred. No. 6.1e-157;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSPSMGR 60
DB 1 MTDVSRKIRAWGRRLMIGTAAAVVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSPSMGR 60
QY 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS 120
DB 61 DIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGQSSFYS 120
QY 121 DWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKTGSAALGLSMAGSSAMILAAAYHP 180
DB 121 DWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKTGSAALGLSMAGSSAMILAAAYHP 180
QY 181 QOFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
DB 181 QOFIYAGSLALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNPTQIIPKL 240
QY 241 VANNTRLWYCGNGTNPNEGNIIPAEFLNFVRSSNLKFQDAYNAAGHNAVFNPPNG 300
DB 241 VANNTRLWYCGNGTNPNEGNIIPAEFLNFVRSSNLKFQDAYNAAGHNAVFNPPNG 300
QY 301 THSWEYWGQAQLNAMKGDLOSSLGAG 325
DB 301 THSWEYWGQAQLNAMKGDLOSSLGAG 325

RESULT 6
US-09-880-505-35
; Sequence 35, Application US/09880505
; Publication No. US20030007976A1

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; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/324,542
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: US 08/997,080
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-09-880-505-35

Query Match 97.8%; Score 1706; DB 11; Length 323;
Best Local Similarity 98.5%; Pred. No. 3e-153;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIWMVPGQSSPYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIWMVPGQSSPYS 120
QY 121 DWSPACGKACQYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
Db 121 DWSPACGKACQYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
QY 181 QOFIYAGSLALLDPSQGMGSLIGLAMDAGGYKAADMWGPSSDPAWERNDTQQIPKL 240
Db 181 QOFIYAGSLALLDPSQGMG--LIGLAMDAGGYKAADMWGPSSDPAWERNDTQQIPKL 238
QY 241 VANNTRLWVYCGNCTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300
Db 239 VANNTRLWVYCGNCTPNELGGANIPAEFLENFVRSSNLKFQDAYKPAGGHNAVFPPNG 298
QY 301 THSWEYGAQINAMKGDLOSSLGAG 325
Db 299 THSWEYGAQINAMKGDLOSSLGAG 323

RESULT 7
US-10-051-643-35
; Sequence 35, Application US/10051643
; Publication No. US20020197265A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
; TITLE OF INVENTION: System using Mycobacterium Vaccae
; FILE REFERENCE: 11000.1008c2
; CURRENT APPLICATION NUMBER: US/10/051,643
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US09/156,181
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 08/996,624
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
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US-10-051-643-35

Query Match 97.8%; Score 1706; DB 14; Length 323;
Best Local Similarity 98.5%; Pred. No. 3e-153;
Matches 320; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
Db 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLQVPSMGR 60
QY 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIWMVPGQSSPYS 120
Db 61 DIKVFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYQSGLSIWMVPGQSSPYS 120
QY 121 DWSPACGKACQYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
Db 121 DWSPACGKACQYKWTETLTSELPOWLSANRAVKPTGSAAGLSWAGSSAMILAAVHP 180
QY 181 QOFIYAGSLALLDPSQGMGSLIGLAMDAGGYKAADMWGPSSDPAWERNDTQQIPKL 240
Db 181 QOFIYAGSLALLDPSQGMG--LIGLAMDAGGYKAADMWGPSSDPAWERNDTQQIPKL 238
QY 241 VANNTRLWVYCGNCTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300
Db 239 VANNTRLWVYCGNCTPNELGGANIPAEFLENFVRSSNLKFQDAYKPAGGHNAVFPPNG 298
QY 301 THSWEYGAQINAMKGDLOSSLGAG 325
Db 299 THSWEYGAQINAMKGDLOSSLGAG 323

RESULT 8
US-09-051-755-16
; Sequence 16, Application US/09051755
; Patent No. US20010018048A1
; GENERAL INFORMATION:
; APPLICANT: LEER, Robert J
; APPLICANT: POWELS, Pieter H
; APPLICANT: CONWAY, Patricia L
; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND FOOD ADDITIVES C
; FILE REFERENCE: LEER et al. 09/051,755
; CURRENT APPLICATION NUMBER: US/09/051,755
; CURRENT FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: PCT/NL95/00367
; EARLIER FILING DATE: 1995-10-20
; EARLIER APPLICATION NUMBER: PCT/NL96/00409
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 16
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:aligned aa
; OTHER INFORMATION: sequence of Mycobacterium Mtu85b
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(364)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-051-755-16

Query Match 92.4%; Score 1612; DB 9; Length 364;
Best Local Similarity 92.6%; Pred. No. 2.9e-144;
Matches 325; Conservative 0; Mismatches 0; Indels 26; Gaps 12;

QY 1 MTDVSRKIRA-----WGRRLMIGTAAAVLPGLVGLAGGAATAGAFSPG-LPVEYLQVPS 55
Db 3 MTDVSRKIRAXXXXXXWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSPGXL-PVEYLQVPS 62
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QY 56 P-SMGRDIKV-QFQSGGNNSPAVYLLDGLRAQDDY--NGWDINTPAFEWYQSG-LSIYV 110
 Db 63 PXSMDRDIKVQFQSGGNNSPAVYLLDGLRAQDDYXXNGWDINTPAFEWYQSGXLSIYV 122
 QY 111 PVGGQSSFYSDWYSPACGKAGCQTYKWET-FLTSELPOWLSANRAVKPTGSAAGL----- 165
 Db 123 PVGGQSSFYSDWYSPACGKAGCQTYKWETXFLTSELPOWLSANRAVKPTGSAAGLXXXX 182
 QY 166 --SMAGSS---AMILAAHYHQPI---YAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 217
 Db 183 XXSMAGSSXXXAMILAAHYHQPIXXXAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 242
 QY 218 DMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTNELGGANIPAEFFENFVRSSN 277
 Db 243 DMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTNELGGANIPAEFFENFVRSSN 302
 QY 278 LKFDQDAYNAAGGHNAVFNPFPNGTHSWE--YMGAGLNAAMKGDLOSSL-GAG 325
 Db 303 LKFDQDAYNAAGGHNAVFNPFPNGTHSWEXXYWGAQLNAMKGDLOSSLXGAG 353
 RESULT 9
 US-10-231-055-16
 ; Sequence 16, Application US/10231055
 ; Publication No. US2003009578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEER, Robert J
 ; APPLICANT: POWELS, Pieter H
 ; APPLICANT: CONWAY, Patricia L
 ; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
 ; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
 ; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND FOOD ADDITIVES C
 ; FILE REFERENCE: LEER et al. 09/051,755
 ; CURRENT APPLICATION NUMBER: US/10/231,055
 ; PRIOR FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: US/09/051,755
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: PCT/NL95/00367
 ; PRIOR FILING DATE: 1995-10-20
 ; PRIOR APPLICATION NUMBER: PCT/NL96/00409
 ; PRIOR FILING DATE: 1996-10-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:aligned aa
 ; OTHER INFORMATION: sequence of Mycobacterium Mtu85b
 ; NAME/KEY: UNSURE
 ; LOCATION: (1)..(364)
 ; OTHER INFORMATION: Xaa is any amino acid.
 US-10-231-055-16
 Query Match 92.4%; Score 1612; DB 15; Length 364;
 Best Local Similarity 92.6%; Pred. No. 2.9e-144;
 Matches 325; Conservative 0; Mismatches 0; Indels 26; Gaps 12;
 QY 1 MTDVSRKIRA-----WGRRLMIGTAAAVLPGLVLAGGAATAGASRPG-LPVEYLQVPS 55
 Db 3 MTDVSRKIRAXXXXWGRRLMIGTAAAVLPGLVLAGGAATAGASRPG-LPVEYLQVPS 62
 QY 56 P-SMGRDIKV-QFQSGGNNSPAVYLLDGLRAQDDY--NGWDINTPAFEWYQSG-LSIYV 110
 Db 63 PXSMDRDIKVQFQSGGNNSPAVYLLDGLRAQDDYXXNGWDINTPAFEWYQSGXLSIYV 122
 QY 111 PVGGQSSFYSDWYSPACGKAGCQTYKWET-FLTSELPOWLSANRAVKPTGSAAGL----- 165
 Db 123 PVGGQSSFYSDWYSPACGKAGCQTYKWETXFLTSELPOWLSANRAVKPTGSAAGLXXXX 182

QY 166 --SMAGSS---AMILAAHYHQPI---YAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 217
 Db 183 XXSMAGSSXXXAMILAAHYHQPIXXXAGSLSALLDPSQGMGPSLIGLAMDAGGYKAA 242
 QY 218 DMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTNELGGANIPAEFFENFVRSSN 277
 Db 243 DMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTNELGGANIPAEFFENFVRSSN 302
 QY 278 LKFDQDAYNAAGGHNAVFNPFPNGTHSWE--YMGAGLNAAMKGDLOSSL-GAG 325
 Db 303 LKFDQDAYNAAGGHNAVFNPFPNGTHSWEXXYWGAQLNAMKGDLOSSLXGAG 353
 RESULT 10
 US-10-369-983-18
 ; Sequence 18, Application US/10369983
 ; Publication No. US20030235593A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Guderian, Jeff
 ; APPLICANT: Reed, Steven
 ; APPLICANT: Corixa Corporation
 ; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 ; FILE REFERENCE: 014058-009081US
 ; CURRENT APPLICATION NUMBER: US/10/369,983
 ; CURRENT FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/357,351
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 1016
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:fusion protein
 ; OTHER INFORMATION: MTB103F (MTB72F-85b)
 US-10-369-983-18
 Query Match 89.9%; Score 1568.5; DB 12; Length 1016;
 Best Local Similarity 94.5%; Pred. No. 1.5e-139;
 Matches 292; Conservative 4; Mismatches 12; Indels 1; Gaps 1;
 QY 18 GTAAAVLPLGLVLAG-CAATAGAFSRPGLPVEYLQVPSMGRDIKVQFQSGGNNSPAV 76
 Db 708 GDSGGPVVNGLGQVVGWMTAASGTSRPLPVEYLQVPSMGRDIKVQFQSGGNNSPAV 767
 QY 77 YLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGSSSFYSDWYSPACGKAGCQTYK 136
 Db 768 YLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGSSSFYSDWYSPACGKAGCQTYK 827
 QY 137 WETFLTSELPOWLSANRAVKPTGSAAGLWAGSSAMILAAHYHQPIYAGSLSALLDPS 196
 Db 828 WETFLTSELPOWLSANRAVKPTGSAAGLWAGSSAMILAAHYHQPIYAGSLSALLDPS 887
 QY 197 QGMGPSLIGLAMDAGGYKAAADMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTP 256
 Db 888 QGMGPSLIGLAMDAGGYKAAADMWGPSSDPAWERNDDTQOIPKLVANNTRLWVYCGNGTP 947
 QY 257 NELGGANIPAEFFENFVRSSNLKFQDAYNAAGGHNAVFNPFPNGTHSWYGAQLNAMKG 316
 Db 948 NELGGANIPAEFFENFVRSSNLKFQDAYNAAGGHNAVFNPFPNGTHSWYGAQLNAMKG 1007
 QY 317 DLQSSLGAG 325
 Db 1008 DLQSSLGAG 1016
 RESULT 11
 US-10-369-983-4
 ; Sequence 4, Application US/10369983
 ; Publication No. US20030235593A1
 ; GENERAL INFORMATION:

```
; APPLICANT: Skeiky, Yasir
; APPLICANT: Guderian, Jeff
; APPLICANT: Reed, Steven
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
; FILE REFERENCE: 014058-009081US
; CURRENT APPLICATION NUMBER: US/10/369,983
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/357,351
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:MTB-102F fusion
; OTHER INFORMATION: protein
US-10-369-983-4

Query Match      89.2%; Score 1557; DB 12; Length 1010;
Best Local Similarity 82.9%; Pred. No. 1.8e-138;
Matches 296; Conservative 3; Mismatches 18; Indels 40; Gaps 2;

QY 9 RAWGRRUMIGTAAAVLVP-----GLVGLAGGAATAGA----- 40
DB 654 QAWAANQAVTPARALPLTSLTSAERGPGQMLGGLPVQMGARAGGSLGVLRVPRP 713

QY 41 -----FSRPGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDY 88
DB 714 YVMPHSPAAGKLFSPRGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDY 773

QY 89 NGWDINTPAFEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOW 148
DB 774 NGWDINTPAFEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOW 833

QY 149 LSNARAVKPTGSAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAM 208
DB 834 LSNARAVKPTGSAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAM 893

QY 209 GDAGGYKAADWGFSSDPAWERNPTQIQPKLVANTRLWYVCGNGTPELGGANIPAEF 268
DB 894 GDAGGYKAADWGFSSDPAWERNPTQIQPKLVANTRLWYVCGNGTPELGGANIPAEF 953

QY 269 LENFVRSSNLKPDAYNAAGHNNAVFPNPGTHSWYWGQAQLNAMKGDLOSSLGAG 325
DB 954 LENFVRSSNLKPDAYNAAGHNNAVFPNPGTHSWYWGQAQLNAMKGDLOSSLGAG 1010

RESULT 12
US-09-791-171-173
; Sequence 173, Application US/09791171
; Patent No. US2002094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 127/97
; PRIOR FILING DATE: 1997-11-10
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; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-173

Query Match      88.8%; Score 1550; DB 9; Length 403;
Best Local Similarity 99.3%; Pred. No. 2.5e-138;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 AGAFSRPGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 97
DB 116 AKLFSPRGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 175

QY 98 FEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKP 157
DB 176 FEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKP 235

QY 158 TGSAAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAMGDAGGYKAA 217
DB 236 TGSAAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAMGDAGGYKAA 295

QY 218 DMGPPSSDPAWERNPTQIQPKLVANTRLWYVCGNGTPELGGANIPAEFLENFVRSSN 277
DB 296 DMGPPSSDPAWERNPTQIQPKLVANTRLWYVCGNGTPELGGANIPAEFLENFVRSSN 355

QY 278 LKFDQAYNAAGHNNAVFPNPGTHSWYWGQAQLNAMKGDLOSSLGAG 325
DB 356 LKFDQAYNAAGHNNAVFPNPGTHSWYWGQAQLNAMKGDLOSSLGAG 403

RESULT 13
US-09-805-427a-4
; Sequence 4, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-805-427A-4

Query Match      88.8%; Score 1550; DB 10; Length 403;
Best Local Similarity 99.3%; Pred. No. 2.5e-138;
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 AGAFSRPGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 97
DB 116 AKLFSPRGLPVEYLQVPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPA 175

QY 98 FEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKP 157
DB 176 FEWYQSGLSIVMPVGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPOWLSANRAVKP 235

QY 158 TGSAAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAMGDAGGYKAA 217
DB 236 TGSAAIGLSMAGSSAMILAAVHPQOFTYAGSLSALLDPSQGMGSLIGLAMGDAGGYKAA 295
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QY 218 DMWGPSSDPAWERNDPTQOIPKLVANNTRLVVYCGNGTNPGLGANNIPAEFFLENFVRSSN 277
 Db 296 DMWGPSSDPAWERNDPTQOIPKLVANNTRLVVYCGNGTNPGLGANNIPAEFFLENFVRSSN 355
 QY 278 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 325
 Db 356 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 403
 RESULT 14
 US-09-804-980-173
 ; Sequence 173, Application US/09804980
 ; Publication No. US20030147897A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Statens Serum Institut
 ; APPLICANT: Anderson, Peter
 ; TITLE OF INVENTION: M. Tuberculosis Antigens
 ; FILE REFERENCE: 670001-2002.4
 ; CURRENT APPLICATION NUMBER: US/09/804,980
 ; CURRENT FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 257
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 173
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-804-980-173

Query Match 88.8%; Score 1550; DB 12; Length 403;
 Best Local Similarity 99.3%; Pred. No. 2.5e-138;
 Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 38 AGAFSPGLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPA 97
 Db 116 AKLFSPGLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPA 175
 QY 98 FEWYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKP 157
 Db 176 FEWYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKP 235
 QY 158 TGSAAIIGLSMAGSSAMILAAHYHPQOPIYAGSLSALLDPSQGMGPSLIGLAMGDAGYKAA 217
 Db 296 DMWGPSSDPAWERNDPTQOIPKLVANNTRLVVYCGNGTNPGLGANNIPAEFFLENFVRSSN 355
 QY 278 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 325
 Db 356 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 403

RESULT 15
 US-09-872-505-4
 ; Sequence 4, Application US/09872505
 ; Publication No. US20040013685A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Statens Serum Institut
 ; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
 ; FILE REFERENCE: 670001-2002.6
 ; CURRENT APPLICATION NUMBER: US/09/872,505
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
 US-09-872-505-4

Query Match 88.8%; Score 1550; DB 12; Length 403;
 Best Local Similarity 99.3%; Pred. No. 2.5e-138;
 Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 38 AGAFSPGLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPA 97
 Db 116 AKLFSPGLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPA 175
 QY 98 FEWYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKP 157
 Db 176 FEWYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKP 235
 QY 158 TGSAAIIGLSMAGSSAMILAAHYHPQOPIYAGSLSALLDPSQGMGPSLIGLAMGDAGYKAA 217
 Db 296 DMWGPSSDPAWERNDPTQOIPKLVANNTRLVVYCGNGTNPGLGANNIPAEFFLENFVRSSN 355
 QY 278 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 325
 Db 356 LKFQDAYNAAGGHNAVFPPNGTHSWYWGAGLNAMKGDLOSSLGAG 403

RESULT 16
 US-09-791-171-172
 ; Sequence 172, Application US/09791171
 ; Patent No. US20020094336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSEN, Peter
 ; APPLICANT: NIELSEN, Rikke
 ; APPLICANT: OETTINGER, Thomas
 ; APPLICANT: RASMUSSEN, Peter Birk
 ; APPLICANT: ROSENKRANDS, Ida
 ; APPLICANT: WELLDINGH, Karin
 ; APPLICANT: FLORIO, Walter
 ; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
 ; FILE REFERENCE: 670001-2002.1
 ; CURRENT APPLICATION NUMBER: US/09/791,171
 ; CURRENT FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 09/050,739
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 0376/97
 ; PRIOR FILING DATE: 1997-04-02
 ; PRIOR APPLICATION NUMBER: 1277/97
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/044,624
 ; PRIOR FILING DATE: 1997-04-18
 ; PRIOR APPLICATION NUMBER: 60/070,488
 ; PRIOR FILING DATE: 1998-01-05
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 172
 ; LENGTH: 404
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-791-171-172

Query Match 88.8%; Score 1550; DB 9; Length 404;
 Best Local Similarity 99.7%; Pred. No. 2.5e-138;
 Matches 285; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 40 AFSRPGPLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPAPE 99
 Db 21 SFSRPGPLPVEYLQVPSMGSDIKVQFQSGGNSPAVYLLDGLRAODDYNWDINTPAPE 80
 QY 100 WYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTG 159
 Db 81 WYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWEFTLTSELPOWLSANRAVKPTG 140
 QY 160 SAAIIGLSMAGSSAMILAAHYHPQOPIYAGSLSALLDPSQGMGPSLIGLAMGDAGYKAA 219

Db 141 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 200
Qy 220 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 279
Db 201 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 260
Qy 280 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 325
Db 261 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 306

RESULT 17

US-09-805-427A-3
; Sequence 3, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805.427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-805-427A-3

Query Match 88.8%; Score 1550; DB 10; Length 404;
Best Local Similarity 99.7%; Pred. No. 2.5e-138;
Matches 285; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 40 AFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 99
Db 21 SFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 80
Qy 100 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 159
Db 81 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 140
Qy 160 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 219
Db 141 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 200
Qy 220 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 279
Db 201 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 260
Qy 280 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 325
Db 261 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 306

RESULT 18

US-09-804-980-172
; Sequence 172, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804.980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-172

Query Match 88.8%; Score 1550; DB 12; Length 404;
Best Local Similarity 99.7%; Pred. No. 2.5e-138;
Matches 285; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 40 AFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 99
Db 21 SFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 80
Qy 100 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 159
Db 81 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 140
Qy 160 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 219
Db 141 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 200
Qy 220 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 279
Db 201 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 260
Qy 280 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 325
Db 261 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 306

RESULT 19

US-09-872-505-3
; Sequence 3, Application US/09872505
; Publication No. US20040013685A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872.505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-872-505-3

Query Match 88.8%; Score 1550; DB 12; Length 404;
Best Local Similarity 99.7%; Pred. No. 2.5e-138;
Matches 285; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 40 AFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 99
Db 21 SFSRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFE 80
Qy 100 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 159
Db 81 WYQSGLSIYMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELQWLSANRAVKPTG 140
Qy 160 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 219
Db 141 SAAIGLSMAGSSAMILAAAYHPQQFIYAGLSALLDPSQGMGSPSLIGLAWGDAGGYKAADM 200
Qy 220 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 279
Db 201 WGPSSDDPAWERNPTQIQIPKLVANNTLWYCGNGTNEELGGANIPAEFFLENFVRSSNLK 260
Qy 280 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 325
Db 261 FQDAYNAAGGHNAVFNPNGTHSWEYWGQALNAMKGDLOSSLGAG 306

RESULT 21

US-09-880-505-31

Sequence 31, Application US/09880505

Publication No. US20030007976A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c2

CURRENT APPLICATION NUMBER: US/09/880,505

CURRENT FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 09/324,542

PRIOR FILING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: US 08/997,080

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 327

TYPE: PRT

ORGANISM: Mycobacterium leprae

US-09-880-505-31

Query Match 83.3%; Score 1454; DB 11; Length 327;

Best Local Similarity 83.0%; Pred. No. 2.3e-129;

Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGR 60

DB 1 MIDVSGKIRAWGRWLLVG--AAATLPSTISLAGGAATASAFRGLPVEYLOVPSMGR 58

QY 61 DIKVOFQSGGNNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGSSFY 120

DB 59 TIKVQFQGGNSPAVYLLDGLRAODDYGNDINTSAFEWYQSGLSIVMPVGGSSFY 118

QY 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180

DB 119 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 178

QY 181 QOFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 240

DB 179 DQFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 238

QY 241 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 300

DB 239 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 298

QY 301 THSWEYGAQLNAMKGDLOSSLGA 324

DB 299 THSWEYGAQLNAMKPDLOTLMA 322

RESULT 22

US-10-051-643-31

Sequence 31, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L. J.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

FILE REFERENCE: 11000.1008c2

CURRENT APPLICATION NUMBER: US/10/051,643

CURRENT FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US09/156,181

PRIOR FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: US 08/996,624

PRIOR FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 208

SOFTWARE: FastSeq for Windows Version 3.0

Query Match 87.2%; Score 1522; DB 11; Length 330;

Best Local Similarity 84.9%; Pred. No. 8.4e-136;

Matches 275; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGR 60

DB 1 MTDLSKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGR 60

QY 61 DIKVOFQSGGNNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGSSFY 120

DB 61 DIKVOFQSGGNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGSSFY 120

QY 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180

DB 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180

QY 181 QOFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 240

DB 181 DQFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 240

QY 241 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 300

DB 241 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 300

QY 301 THSWEYGAQLNAMKGDLOSSLGA 324

DB 301 THSWEYGAQLNAMKPDLOTLMA 324

RESULT 20

US-09-952-554-2

Sequence 2, Application US/09952554

Publication No. US20030036104A1

GENERAL INFORMATION:

APPLICANT: Wallis, Robert S.

TITLE OF INVENTION: DETECTION OF MYCOBACTERIA

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patencin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/952,554

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/690,347

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: CASE-02270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 330 amino acids

TYPE: amino acid

STRANDEDNESS: No. US20030036104A1 Relevant

TOPOLOGY: No. US20030036104A1 Relevant

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-952-554-2

Query Match 87.2%; Score 1522; DB 11; Length 330;

Best Local Similarity 84.9%; Pred. No. 8.4e-136;

Matches 275; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTDVSRKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGR 60

DB 1 MTDLSKIRAWGRRLMIGTAAAVLPGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGR 60

QY 61 DIKVOFQSGGNNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGSSFY 120

DB 61 DIKVOFQSGGNSPAVYLLDGLRAODDYGNDINTPAFEWYQSGLSIVMPVGGSSFY 120

QY 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180

DB 121 DWYSPACGKAGCQTYKWTFTLTSELPQWLSANRAVKPTGSAAGLSMAGSSAMILAAHP 180

QY 181 QOFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 240

DB 181 DQFIYAGSLSDLPSCQMGPSLIGLAMDAGGYKAADMWGPSSDPANERNDPTQOIPKL 240

QY 241 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 300

DB 241 VANNTRLWYCGNGTPELGGANIPAEFLNFVRSSNLKFODAYNAAGHNVAFFPENG 300

QY 301 THSWEYGAQLNAMKGDLOSSLGA 324

DB 301 THSWEYGAQLNAMKPDLOTLMA 324

```
; SEQ ID NO 31
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-051-643-31

Query Match      83.3%; Score 1454; DB 14; Length 327;
Best Local Similarity 83.0%; Pred. No. 2.3e-129;
Matches 269; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MTIVSRKIRAWGRMLMTGTAARVLPGLVGLAGGAATAGAFSPRLPVEYLQVPSMGR 60
Db 1 MIDVSGKIRAWGRLLVG--AAATPLSLISLAGGAATASAFSPRLPVEYLQVPSMGR 58
QY 61 DIKVFQSGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFSYS 120
Db 59 TIKVFQSGGNSPAVLLDGLRAQDDYNGWDINTSAFEWYQSGLSIVMPVGGSSFSYS 118
QY 121 DWYSPACGKAGCQTYKWETFLTSELTPQLWLSANRAVKPTGSAAGLSMAGSSAMILAAHYHP 180
Db 119 DWYSPACGKAGCQTYKWETFLTSELTPKWSANRSVKSTGSAVVGSLMAGSSAMILAAHYHP 178
QY 181 QOFIYAGSLALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPQQIPKL 240
Db 179 DQFIYAGSLALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPQQIPKL 238
QY 241 VANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 300
Db 239 VANNTRLWVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNG 298
QY 301 THSWEYWGALNAMKGDLOSSLGA 324
Db 299 THSWEYWGALNAMKPDLOSSLGA 322

RESULT 23
US-09-880-505-32
; Sequence 32, Application US/09880505
; Publication No. US20030007976A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c2
; CURRENT APPLICATION NUMBER: US/09/880,505
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 1999-06-02
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-880-505-32

Query Match      80.6%; Score 1407; DB 11; Length 338;
Best Local Similarity 78.9%; Pred. No. 6.9e-125;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0;

QY 8 IRAWGRMLMTGTAARVLPGLVGLAGGAATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 67
Db 11 VTGMSRRLVVGAVGAALVSLGVAVGCTATAGAFSPRLPVEYLQVPSMGRDIKVQFQ 70
QY 68 SGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFSYSFSDWYSPAC 127
Db 71 SGGNSPAVLLDGLRAQDDYNGWDINTPAFEWYQSGLSIVMPVGGSSFSYSFSDWYSPAC 130
QY 128 GKAGCQTYKWETFLTSELTPQLWLSANRAVKPTGSAAGLSMAGSSAMILAAHYHPQFQIYAG 187
Db 131 GKAGCQTYKWETFLTSELTPQLWLSANRAVKPTGSAAGLSMAGSSAMILAAHYHPQFQIYAG 190
QY 188 SLSALLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPQQIPKL VANNTRL 247
Db 191 AMSGLLDPSQMGPSLIGLAMGDAGGYKAADMWGPSSDPDAWERNDPQQIPKL VANNTRL 250
QY 248 WVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNGTHSWEYW 307
Db 251 WVYCGNGTPELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFPPNGTHSWEYW 310
QY 308 GAQLNAMKGDLOSSLGA 324
Db 311 GAQLNAMKPDLOSSLGA 327

RESULT 25
US-10-051-643-32
; Sequence 32, Application US/10051643
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; ORGANISM: Mycobacterium bovis
US-10-051-643-34

Query Match      80.6%; Score 1407; DB 14; Length 338;
Best Local Similarity 78.9%; Pred. No. 6.9e-125;
Matches 250; Conservative 29; Mismatches 38; Indels 0; Gaps 0

Qy 8 IRWGRRLMIGTAAAVLVPLGLVLAGGAATAGAFSRPGLPVEYLQVPSPSMRDIKVQFQ 67
Db 11 VTCMSRLVLVGAVALVSLGLVAVGCTATAGAFSRPGLPVEYLQVPSPSMRDIKVQFQ 70
Qy 68 SGGNNSPAVLLDGLRAQDDYNGWDINTPAPEWYYSGLSLVMPVGGSSYSYDWSYAC 127
Db 71 SGGANSFALYLLDGLRAQDDPSFGWDINTPAPEWYDQSLSYMPVGGSSYSYDWPAC 130
Qy 128 GKAGCQTYKWEFTLTSELPOWLSANRAVKPTGSAAGLSMAGSSAMILLAAVHPQOFIYAG 187
Db 131 GKAGCQTYKWEFTLTSELPGWLQANRHVKPTGSAVUGLSMAASALTIAIYHPQOFIYAG 190
Qy 188 SLSALLDPSQMGPSLIGLAMDAGGYKAADMWGPSSDPAPERNDPTQOIPKLVANNTRL 247
Db 191 AMSGLLDPSQMGPTLIGLAMDAGGYKASDMWGPCKEDPAQRNDPLINVGKLIANNTRV 250
Qy 248 WYVCGNCTPNELGGANIPAEFLENFVSSNLKFODAYNAGGHNAVFNPENGTHSWEYW 307
Db 251 WYVCGNCKPSDLGGNNLPAPKLEGFVETSNIKFODAYNAGGHNGVDFDPDGGTHSWEYW 310
Qy 308 GAQLNAMKGDLOQSSIGA 324
Db 311 GAQLNAMKPDLORALGA 327

RESULT 27
US-09-051-755-17
; Sequence 17, Application US/09051755
; Patent No. US200100180481
; GENERAL INFORMATION:
; APPLICANT: LEEB, Robert J
; APPLICANT: FOUWELS, Pieter H
; APPLICANT: CONWAY, Patricia L
; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND FOOD ADDITIVES C
; FILE REFERENCE: LEEB et al. 09/051,755
; CURRENT APPLICATION NUMBER: US/09/051,755
; CURRENT FILING DATE: 1998-09-30
; EARLIER APPLICATION NUMBER: PCT/NL95/00367
; EARLIER FILING DATE: 1995-10-20
; EARLIER APPLICATION NUMBER: PCT/NL96/00409
; EARLIER FILING DATE: 1996-10-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 364
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: aligned aa
; OTHER INFORMATION: sequence of Mycobacterium Mlep85b
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(364)
; OTHER INFORMATION: Xaa is any amino acid.
US-09-051-755-17

```

Qy 56 P-SWGRDIKV-QFQSGGNNSPAVYLLDGLRAQDDY--NGWDINTPAPEWYQSG-LSIVM 110
 Db 63 EXAMGRTIKVXQFQNGGNGSPAVYLLDGLRAQDDYXXNGWDINTSAPEWYQSGXLSVVM 122
 Qy 111 PVGQSSFYSDWYSPACGKAGCQTYKWET-FLTSELPOWLSANRAVKPTGSAATGL----- 165
 Db 123 PVGQSSFYSDWYSPACGKAGCQTYKWETXFLTSELPKWLSANRSVKSTGSAVVGLXXXX 182
 Qy 166 --SWAGSS---AMILAAHPQOFI---YAGSLALLDPSQGMGSPSLIGLAMGDAGGYKAA 217
 Db 183 XXSWAGSSXXXALILAAHPDQFIXXYAGSLALMDSSQGIIEPOLIGLAMGDAGGYKAA 242
 Qy 218 DMWGSPSDPAWERNPTQOIPKLVANTRLWVYCGNTPNELGANTPAEFLENFVRSN 277
 Db 243 DMWGPPNDPAWQRNDPILOAGKLVANNTLWVYCGNTPSELGCTNVPABFLENFVHGSN 302
 Qy 278 LKQDAYNAAGGHNVAFFPNPNGTHSWE--YWGAQLNAMKGDQLQSSL 322
 Db 303 LKQDAYNGAGGHNVAFFNLNADGTHSWEXXYWGQAQLNAMKPDQLNTL 349

RESULT 28

US-10-231-055-17
 ; Sequence 17, Application US/10231055
 ; Publication No. US20030095978A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEER, Robert J
 ; APPLICANT: POWELS, Patricia L
 ; TITLE OF INVENTION: NOVEL ADHERENCE FACTORS OF NON PATHOGENIC
 ; TITLE OF INVENTION: MICROORGANISMS AND APPLICATIONS THEREOF FOR SCREENING
 ; TITLE OF INVENTION: MICROORGANISMS FOR SPECIFIC PROBIOTIC PROPERTIES; NOVEL
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND FOOD ADDITIVES C
 ; FILE REFERENCE: LEER et al. 09/051,755
 ; CURRENT APPLICATION NUMBER: US/10/231,055
 ; PRIOR FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: US/09/051,755
 ; PRIOR FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: PCT/NL95/00367
 ; PRIOR FILING DATE: 1995-10-20
 ; PRIOR APPLICATION NUMBER: PCT/NL96/00409
 ; PRIOR FILING DATE: 1996-10-21
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 17
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:aligned aa
 ; OTHER INFORMATION: sequence of Mycobacterium Mlep85b

Qy 1 MTDVSRKTRA---WGRRLMTGTAADVLPGLVGLAGGAATAGAFSRPG-LPVEYLOVPS 55
 Db 3 MIDVSGKIRAXXXKRWRLVGLGAATXXLPGLSLIAGGAATASAFSRPGLPVEYLOVPS 62
 Qy 56 P-SWGRDIKV-QFQSGGNNSPAVYLLDGLRAQDDY--NGWDINTPAPEWYQSG-LSIVM 110
 Db 63 EXAMGRTIKVXQFQNGGNGSPAVYLLDGLRAQDDYXXNGWDINTSAPEWYQSGXLSVVM 122
 Qy 111 PVGQSSFYSDWYSPACGKAGCQTYKWET-FLTSELPOWLSANRAVKPTGSAATGL----- 165
 Db 123 PVGQSSFYSDWYSPACGKAGCQTYKWETXFLTSELPKWLSANRSVKSTGSAVVGLXXXX 182

Query Match

Best Local Similarity 76.8%; Score 1339.5; DB 15; Length 364;
 Matches 268; Conservative 19; Mismatches 35; Indels 25; Gaps 11;

Qy 1 MTDVSRKTRA---WGRRLMTGTAADVLPGLVGLAGGAATAGAFSRPG-LPVEYLOVPS 55
 Db 3 MIDVSGKIRAXXXKRWRLVGLGAATXXLPGLSLIAGGAATASAFSRPGLPVEYLOVPS 62
 Qy 56 P-SWGRDIKV-QFQSGGNNSPAVYLLDGLRAQDDY--NGWDINTPAPEWYQSG-LSIVM 110
 Db 63 EXAMGRTIKVXQFQNGGNGSPAVYLLDGLRAQDDYXXNGWDINTSAPEWYQSGXLSVVM 122
 Qy 111 PVGQSSFYSDWYSPACGKAGCQTYKWET-FLTSELPOWLSANRAVKPTGSAATGL----- 165
 Db 123 PVGQSSFYSDWYSPACGKAGCQTYKWETXFLTSELPKWLSANRSVKSTGSAVVGLXXXX 182

Qy 166 --SWAGSS---AMILAAHPQOFI---YAGSLALLDPSQGMGSPSLIGLAMGDAGGYKAA 217
 Db 183 XXSWAGSSXXXALILAAHPDQFIXXYAGSLALMDSSQGIIEPOLIGLAMGDAGGYKAA 242
 Qy 218 DMWGSPSDPAWERNPTQOIPKLVANTRLWVYCGNTPNELGANTPAEFLENFVRSN 277
 Db 243 DMWGPPNDPAWQRNDPILOAGKLVANNTLWVYCGNTPSELGCTNVPABFLENFVHGSN 302
 Qy 278 LKQDAYNAAGGHNVAFFPNPNGTHSWE--YWGAQLNAMKGDQLQSSL 322
 Db 303 LKQDAYNGAGGHNVAFFNLNADGTHSWEXXYWGQAQLNAMKPDQLNTL 349

RESULT 29

US-09-880-505-30
 ; Sequence 30, Application US/09880505
 ; Publication No. US20030007976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Tan, Paul L.J.
 ; APPLICANT: Prestidge, Ross
 ; TITLE OF INVENTION: Methods and Compounds for the Treatment
 ; TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
 ; FILE REFERENCE: 11000.1007C2
 ; CURRENT APPLICATION NUMBER: US/09/880,505
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 09/324,542
 ; PRIOR FILING DATE: 1999-06-02
 ; PRIOR APPLICATION NUMBER: US 08/997,080
 ; PRIOR FILING DATE: 1997-12-23
 ; NUMBER OF SEQ ID NOS: 194
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium leprae
 ; US-09-880-505-30

Query Match 76.5%; Score 1335.5; DB 11; Length 330;
 Best Local Similarity 76.6%; Pred. No. 4e-118;
 Matches 239; Conservative 31; Mismatches 41; Indels 1; Gaps 1;

Qy 13 RRLMIGTAAAVLPLGLVGLAGGAATAGAFSRPGLPVEYLOVPSMGRDIKVQFQSGNN 72
 Db 16 RRLVVEAMGVALLSALIGVV-GSAPAEAFSRPGLPVEYLOVPSMGRDIKVQFQSGAN 74
 Qy 73 SPAYLLDGLRAQDDYNGWDINTPAPEWYQSGLSIYMPVGGQSSFYSDWYSPACGKAGC 132
 Db 75 SPALYLLDGLRAQDDDFSGWDINTTAFEWYQSGISVVMVPGQSSFYSDWYSPACGKAGC 134
 Qy 133 QTYKWETFLTSELPOWLSANRAVKPTGSAALGLSMAGSSAMILAAHPQFIYAGSLAL 192
 Db 135 QTYKWETFLTSELPEYLOQSNKQIKPTGSAAVGLSMAGLSALTALAIYHPDQFIYVGSML 194
 Qy 193 LDPSQGMGSPSLIGLAMGDAGGYKAADMWGPPSSDPAWERNPTQOIPKLVANTRLWVYCG 252
 Db 195 LDPSNMGSPSLIGLAMGDAGGYKAADMWGSTDPARKNDEPTVNVGTLIANTRLWVYCG 254
 Qy 253 NGTPELGGANI PAEFLFENFVRSNLFQDAYNAAGGHNVAFFNPPTNGTHSWEYWGQALN 312
 Db 255 NGKPELGGNNLPKLLGLEGLVRTSNIKFQDGYNAGGHNVAFFNPDSGTHSWEYWGQALN 314
 Qy 313 AMKGDQLQSLGA 324
 Db 315 DMKPDLOQYLGA 326

RESULT 30

US-10-051-643-30
 ; Sequence 30, Application US/10051643
 ; Publication No. US20020197265A1
 ; GENERAL INFORMATION:

Search completed: February 5, 2004, 17:43:19
Job time : 45.881 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 5, 2004, 17:25:12 ; Search time 16.9643 Seconds
(without alignments)
888.869 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQQWNFAGTEAASAIQ.....ISEAGQMASTEGNVTGMFA 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1078588

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

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1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	479	100.0	95	16	AAW11494
2	479	100.0	95	20	AAV29890
3	479	100.0	95	20	AAV29788
4	479	100.0	95	22	ABG35219
5	479	100.0	95	23	ABG30968
6	479	100.0	95	23	AAW50740
7	479	100.0	196	20	AAV29888
8	479	100.0	403	19	AAW72943
9	479	100.0	403	20	AAV21963
10	479	100.0	404	20	AAV21962
11	479	100.0	404	20	AAV21962
12	259	54.1	51	18	AAW32466
13	259	54.1	51	18	AAW32339
14	259	54.1	51	19	AAW81701
15	259	54.1	51	19	AAW64334
16	259	54.1	51	20	AAV39131
17	259	54.1	51	20	AAV38988
18	259	54.1	51	22	AAU01897
19	259	54.1	51	23	AAE29716
20	259	54.1	51	23	AAE17580
21	186	38.8	95	23	ABU05360
22	151	31.5	96	22	AAV30391
23	106	22.1	20	18	AAW35547
24	106	22.1	20	21	AAV88580
25	101	21.1	20	22	AAE12275
26	98	20.5	20	22	AAE12277
27	98	20.5	96	20	AAV21964
28	97	20.3	20	22	AAE12276
29	96	20.0	19	18	AAW35548
30	87	18.2	17	21	AAV88581
31	86.5	18.1	100	22	AAV35229
32	85	17.7	96	19	AAW2884
33	85	17.7	96	20	AAV21901
34	85	17.7	96	22	AAV35220
35	85	17.7	96	23	ABU05727
36	81.5	17.0	108	22	AAV30390
37	81	16.9	15	21	AAV94537
38	81	16.9	15	23	ABG30959
39	81	16.9	15	23	ABG30960
40	81	16.9	15	23	ABG30961
41	81	16.9	15	24	ABG75863
42	81	16.9	96	23	ABU05648
43	80.5	16.8	90	22	AAV35233
44	80	16.7	317	8	AAV70303
45	80	16.7	369	8	AAV70309
46	80	16.7	387	8	AAV70307
47	80	16.7	395	8	AAV70308
48	80	16.7	414	8	AAV70313
49	80	16.7	425	8	AAV70315
50	80	16.7	447	8	AAV70344
51	80	16.7	498	8	AAV70302
52	80	16.7	498	22	AAV49641
53	80	16.7	500	17	AAV90303
54	79	16.5	15	21	AAV94590
55	79	16.5	15	21	AAV94592
56	79	16.5	15	23	ABG30951
57	79	16.5	15	23	ABG30962
58	79	16.5	15	23	AAO17432
59	78.5	16.4	368	20	AAV32069
60	78.5	16.4	368	23	AAV4598
61	78.5	16.4	600	20	AAV32068
62	78.5	16.4	600	23	AAU74597
63	78	16.3	15	21	AAV94596
64	78	16.3	15	23	ABG30957
65	77.5	16.2	125	22	AAV35230
66	77	16.1	15	21	AAV94595
67	77	16.1	15	23	ABG30952
68	77	16.1	15	23	AAO17433
69	77	16.1	876	23	ABP65529
70	76.5	16.0	837	22	AAU34387
71	76.5	16.0	875	22	AAU37487
72	76.5	16.0	2434	22	AAU34339
73	76.5	16.0	6281	22	AAU37403
74	76.5	16.0	10498	24	ABU19119
75	76	15.9	15	23	ABG30958
76	76	15.9	16	22	AAE12278
77	76	15.9	424	22	AAU47141
78	74	15.4	15	21	AAV94598
79	74	15.4	15	23	ABG30955
80	74	15.4	15	23	ABG30967
81	74	15.4	166	22	ABG04606
82	73.5	15.3	772	23	ABP30556

Mycobacterium tube
Amino acid sequenc
Mycobacterium tube
Mycobacterium tube
M. tuberculosis im
Mycobacterium tube
M. tuberculosis ES
M. tuberculosis re
Mycobacterium tube
Mycobacterium spec
M. tuberculosis an
C glutamicum prote
ESAT-6 antigen SEQ
Antigenic C-termin
Mycobacterium tube
Amino acid sequenc
Mycobacterium tube
ESAT-6 antigen SEQ
Antigenic N-termin
M tuberculosis RV3
Mycobacterium tube
Amino acid sequenc
M tuberculosis RV0
M. tuberculosis an
C glutamicum prote
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
M. tuberculosis an
M tuberculosis RV3
Sequence of flagel
Sequence of flagel
Sequence of flagel
Sequence of flagel
Sequence of flagel
Sequence of flagel
Escherichia coli H
Thioredoxin-flagel
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Early secreted ant
Mycobacterium tube
Antigenic fusion p
Mycobacterium tube
Mycobacterium tube
M tuberculosis RV3
Mycobacterium tube
Early secreted ant
Bifidobacterium lo
Staphylococcus aur
Staphylococcus aur
Staphylococcus aur
Pathogen specific
Mycobacterium tube
Mycobacterium tube
Propionibacterium
Mycobacterium tube
Mycobacterium tube
Mycobacterium tube
Novel human diagno
Streptococcus poly

83 Streptococcus poly
84 Mycobacterium tube
85 Staphylococcus aur
86 Staphylococcus melano
87 Staphylococcus aur
88 Mycobacterium tube
89 Mycobacterium sp.
90 Mycobacterium spec

83 73.5 15.3 811 23 ABP27026
84 73 15.2 15 23 ABG30956
85 73 15.2 2086 22 AAU34143
86 73 15.2 2470 22 ABB61247
87 73 15.2 5795 22 AAU37017
88 72.5 15.1 299 20 AAY32067
89 72.5 15.1 299 23 AAE29723
90 72.5 15.1 299 23 AAE17587

ALIGNMENTS

RESULT 1
AAW11494
ID AAW11494 standard; Protein; 95 AA.
XX AC AAW11494;
XX DT 27-MAR-1997 (first entry)
XX DE ESAT6.
XX KW ESAT6; Mycobacterium tuberculosis; 6kDa antigen; tuberculosis complex;
XX KW HYB76-8 reactive antigen; interferon-gamma; memory T-lymphocyte; vaccine;
XX KW M. africanum; M. bovis; delayed-type hypersensitivity reaction; therapy.
XX OS Mycobacterium tuberculosis.
XX PN WO9501441-A1.
XX PD 12-JAN-1995.
XX PF 01-JUL-1994; 94WO-DK00273.
XX PR 02-JUL-1993; 93DK-0000798.
XX PA (STAT-) STATENS SERUMINSTITUT.
XX PI Andersen AB, Andersen P, Haslov K, Sorensen A;
XX WPI; 1995-061005/08.
XX DR N-PSDB; AAT51422.
XX Vaccine for tuberculosis induces interferon-gamma release from
PT T-lymphocytes - comprises an antigen released from mycobacteria,
PT for immunisation of humans
XX Claim 5; Page 61-63; 101pp; English.
XX This sequence represents the Mycobacterium tuberculosis ESAT6. ESAT6 is
CC also known as the 6kDa antigen, or the HYB76-8 reactive antigen. ESAT6
CC is released from metabolising bacteria, and can be isolated from short
CC term filtrates grown as shaken cultures for 7 days. ESAT6 also induces a
CC release of interferon-gamma from reactivated memory T-lymphocytes. This
CC protein sequence is included in the vaccine of the invention. The
CC vaccine is for immunising an animal (including humans) against
CC tuberculosis caused by a Mycobacterium belonging to the tuberculosis
CC complex. The Mycobacterium of the tuberculosis complex are, M.
CC tuberculosis, M. africanum, and M. bovis. The vaccine can evoke a
CC protective immune response against tuberculosis or a delayed-type
CC hypersensitivity reaction. The protein can also be included in a
CC composition for diagnosing tuberculosis. The composition is injected
CC intradermally, and a skin reaction is an indicator of tuberculosis.
XX Sequence 95 AA;

Query Match 100.0%; Score 479; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTEQWNFAGIEAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKWD 60
|||||

Db 1 MTEQWNFAGIEAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKWD 60
Qy 61 TATELNALONLARTISEAGQAMASTEGNVTGMFA 95
Db 61 TATELNALONLARTISEAGQAMASTEGNVTGMFA 95

RESULT 2
AAY29890
ID AAY29890 standard; Protein; 95 AA.
XX AC AAY29890;
XX DT 18-NOV-1999 (first entry)
XX DE Mycobacterium tuberculosis ESAT-6 protein sequence.
XX KW Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
XX KW delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
XX KW interferon-gamma release.
XX OS Mycobacterium tuberculosis.
XX PN WC9945119-A2.
XX PD 10-SEP-1999.
XX PF 05-MAR-1999; 99WO-DK00109.
XX PR 06-MAR-1998; 98DK-0000306.
XX PR 06-MAR-1998; 98US-0077105.
XX PA (STAT-) STATENS SERUM INST.
XX PI Jensen CL, Folkersen J;
XX WPI; 1999-551043/46.
XX DR N-PSDB; AAZ21132.
XX New mycobacterial polypeptide produced in lactic acid bacteria, useful
PT in tuberculosis diagnosis and vaccines -
XX Disclosure; Page 75-76; 76pp; English.

XX The present invention describes a bioactive polypeptide (or
CC immunologically equivalent analogue) produced in lactic acid bacteria
CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
CC polypeptide and ESAT-6 polypeptides are useful in compositions for
CC diagnosis of and vaccination against tuberculosis caused by
CC M. tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used
CC to diagnose ongoing/previous sensitisation with these bacteria by
CC detecting cytokine release when contacting blood samples with the
CC polypeptide. The bioactive polypeptide may be used in diagnostic
CC compositions and vaccines for mycobacteria other than of the
CC M. tuberculosis complex, e.g. M. avium which infects poultry and
CC occasionally humans. M. leprae; they are especially useful when they do
CC not react with lymphoid cells previously primed with M. tuberculosis
CC complex mycobacteria, and so do not give rise to a diagnostic reaction
CC in individuals infected with these bacteria. The polypeptides may also
CC be used in vitro diagnostic tests e.g. stimulation of interferon-gamma
CC release from lymphocytes. The polypeptide has similar or higher
CC bioactivity as currently used tuberculin reagent in the standard
CC delayed type hypersensitivity (DTH) skin test for tuberculosis, but may
CC have greater specificity, being better able to discriminate between
CC lymphoid cells primed from tuberculosis and from previous vaccination.
CC The present sequence represents M. tuberculosis ESAT-6 used in the
CC exemplification of the present invention.

Sequence 95 AA;

Query Match 100.0%; Score 479; DB 20; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 Db 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 Db 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 3
 AAY29788
 ID AAY29788 standard; Protein; 95 AA.
 XX
 AC AAY29788;
 XX
 DT 08-NOV-1999 (first entry)
 XX
 DE Mycobacterial tuberculosis ESAT-6 protein.
 XX
 KW Mycobacterial; ESAT-6; 6 kDa antigen; tuberculosis; infection;
 KW immunological response; diagnosis; vaccine.
 XX
 OS Mycobacterium tuberculosis.
 XX
 FN US5955077-A.
 XX
 PD 21-SEP-1999.
 XX
 PF 05-JUN-1995; 95US-0465640.
 XX
 PR 05-JUN-1995; 95US-0465640.
 PR 20-SEP-1993; 93US-0123182.
 PR 01-JUL-1994; 94WO-DK00273.
 XX
 PA (STAT-) STATENS SERUMINSTITUT.
 XX
 PI Andersen AB, Andersen P, Haslov K, Sorensen AL;
 XX
 DR WPI; 1999-539545/45.
 DR N-PSDB; AAZ08877.
 XX
 PT Polypeptide secreted from Mycobacterium is useful as a vaccine
 PT against tuberculosis
 XX
 PS Claim 24; Fig 10C; 39pp; English.
 XX
 CC The present invention describes a purified or non-naturally occurring
 CC polypeptide (I) released from a metabolising mycobacteria comprising an
 CC ESAT6, also called the 6 kDa antigen. The present sequence represents
 CC Mycobacterium tuberculosis ESAT-6 protein. Also described is a purified
 CC or non-naturally occurring polypeptide (II) with the ability to elicit
 CC a delayed type hypersensitivity reaction which comprises a T cell
 CC epitope of (I). (II) can be used with a carrier or vehicle in a
 CC composition for diagnosing tuberculosis caused by mycobacteria belonging
 CC to the tuberculosis complex, i.e. Mycobacterium tuberculosis, M. bovis
 CC and M. africanum. The composition can be used to detect microbial
 CC antibodies or components of mycobacteria in samples or in animals
 CC through the use of immunoassays. (II) can be used as a vaccine for
 CC immunising an animal, including humans against tuberculosis caused by
 CC mycobacteria of the tuberculosis complex. (II) induce a release of
 CC IFN-gamma from reactivated T-lymphocytes evoking a protective immune
 CC response. Vaccine containing (II) has the same protective potency as
 CC the live BCG vaccine against tuberculosis.
 XX
 SQ Sequence 95 AA;

Query Match 100.0%; Score 479; DB 20; Length 95;
 Best Local Similarity 100.0%; Pred. No. 3.3e-44;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 Db 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 Db 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 5
 ABG30968
 ID ABG30968 standard; Protein; 95 AA.
 XX
 AC ABG30968;
 XX

Db 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 Db 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 4
 AAB35219
 ID AAB35219 standard; Protein; 95 AA.
 XX
 AC AAB35219;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE M tuberculosis Rv3875 protein.
 XX
 KW Tuberculosis; TB; vaccine; esat-6 gene family; Rv0287; Rv1036c;
 KW Rv1037c; Rv2348c; Rv2348c; Rv2653c; Rv2654c; Rv3020c; Rv3444c;
 KW Rv3445c; Rv3890c; Rv3891c; Rv3904c; Rv3905c.
 OS Mycobacterium tuberculosis.
 XX
 FN WO200104151-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-DK00398.
 XX
 PR 13-JUL-1999; 99DK-0001020.
 PR 15-JUL-1999; 99US-0144011.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 PI Andersen P, Skjot R;
 XX
 DR WPI; 2001-091923/10.
 XX
 PT New polypeptide encoded by a member of the esat-6 gene family for
 PT immunizing against and diagnosis of tuberculosis -
 XX
 PS Example 2; Page 65; 80pp; English.
 XX
 CC The present invention provides the protein and coding sequences for
 CC members of the esat-6 gene family from Mycobacterium tuberculosis. These
 CC proteins include Rv0287, Rv1036c, Rv1037c, Rv2348c, Rv2348c, Rv2653c,
 CC Rv2654c, Rv3020c, Rv3444c, Rv3445c, Rv3890c, Rv3891c, Rv3904c and
 CC Rv3905c. These can be used to produce vaccines against, and in the
 CC diagnosis of, tuberculosis (TB) infection. The present sequence is one of
 CC the proteins of the invention.
 XX
 SQ Sequence 95 AA;

Query Match 100.0%; Score 479; DB 22; Length 95;
 Best Local Similarity 100.0%; Pred. No. 3.3e-44;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 Db 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 Db 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 5
 ABG30968
 ID ABG30968 standard; Protein; 95 AA.
 XX
 AC ABG30968;
 XX

DT 21-OCT-2002 (first entry)
 XX Mycobacterium tuberculosis ESAT-6.
 DE
 XX
 XX
 KW ESAT-6; mycobacterial infection; tuberculosis; pulmonary tuberculosis;
 KW tuberculosis lymphadenitis; extrapulmonary tuberculosis.
 XX
 OS Mycobacterium tuberculosis.
 XX WO200254072-A2.
 XX
 XX
 XX 11-JUL-2002.
 XX
 XX
 XX 08-JAN-2002; 2002WO-GB000055.
 XX
 XX 08-JAN-2001; 2001GB-0000432.
 XX 08-JAN-2001; 2001US-259868P.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Lalvani A;
 XX
 XX WPI; 2002-583633/62.
 XX
 XX Determining the progress of a mycobacterial infection, by direct ex
 XX vivo quantitation of ESAT-6-specific T cells -
 XX
 XX Disclosure; Page 42; 53pp; English.
 XX
 XX The invention describes a method of determining the efficacy of treatment
 XX for mycobacterial infection (such as pulmonary tuberculosis, tuberculosis
 XX lymphadenitis and extrapulmonary tuberculosis). The method involves
 XX determining the level of T cells specific for a mycobacterial antigen
 XX that has decreased after the treatment and therefore determining the
 XX efficacy of the treatment. The method is useful for determining the
 XX efficacy of treatment for mycobacterial infection, the mycobacterial
 XX infection is Mycobacterium tuberculosis or M. bovis infection. The
 XX invention also describes a method useful for determining the presence of
 XX a latent infection in a sample from the individual for the presence of T
 XX cells specific for a mycobacterial antigen. Also described in a method
 XX for determining the effect of an intervention on a mycobacterial
 XX infection in an individual an a method for treating an individual
 XX infected by a mycobacterium. This is the amino acid sequence of
 XX Mycobacterium tuberculosis ESAT-6, the mycobacterial antigen measured in
 XX the invention.
 XX
 XX Sequence 95 AA;
 XX
 XX Query Match 100.0%; Score 479; DB 23; Length 95;
 XX Best Local Similarity 100.0%; Pred. No. 3.3e-44;
 XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 DB 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 DB 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 RESULT 6
 ID AAM50740 standard; Protein; 95 AA.
 XX
 XX AAM50740;
 XX
 XX 18-APR-2002 (first entry)
 XX Mycobacterium tuberculosis immunodominant Mtb protein ESAT6.
 XX Mtb; ESAT6; immunogen; mycobacteria; immunisation; vaccine.
 XX

OS Mycobacterium tuberculosis.
 XX WO200204018-A2.
 XX
 XX 17-JAN-2002.
 XX
 XX 10-JUL-2001; 2001WO-US21717.
 XX
 XX 10-JUL-2000; 2000US-217646P.
 XX
 XX (COLS) UNIV COLORADO STATE RES FOUND.
 XX Orme IM, Belisle JT;
 XX WPI; 2002-164602/21.
 XX
 XX Vaccine for boosting immunity to mycobacteria when administered in
 XX mid-life in a subject who has been vaccinated in childhood with
 XX Bacillus Calmette-Guerrin, has purified proteins from mycobacterium
 XX tuberculosis -
 XX
 XX Claim 8; Page 18; 61pp; English.
 XX
 XX The present sequence is that of the Mycobacterium tuberculosis
 XX (Mtb) strain H37Rv gene Rv3875 product, designated ESAT6. This
 XX is one of 31 immunodominant secreted or cytosolic Mtb proteins
 XX of strain H37Rv (see AAM50729-59) discovered through the use of
 XX 2-dimensional liquid phase electrophoresis coupled with an in vitro
 XX interferon-gamma assay and liquid chromatography-mass spectrometry.
 XX The immunogens stimulate a strong interferon-gamma response from
 XX T cells of M. tuberculosis infected mice. The invention provides
 XX vaccine compositions for boosting immunity to mycobacteria when
 XX administered in mid-life to a subject who has been vaccinated
 XX neonatally or in early childhood with BCG and in whom protective
 XX immunity has waned. The vaccine compositions comprise 1 or more
 XX of the 31 purified immunogenic proteins. When used as immunogens,
 XX the secreted Mtb proteins lack the secreted signal sequence. A
 XX preferred protein is Ag85A (see AAM50759), the secreted product of
 XX the Rv3084v gene.
 XX
 XX Sequence 95 AA;
 XX
 XX Query Match 100.0%; Score 479; DB 23; Length 95;
 XX Best Local Similarity 100.0%; Pred. No. 3.3e-44;
 XX Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 DB 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 DB 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 RESULT 7
 ID AAY29888 standard; Protein; 196 AA.
 XX
 XX AAY29888;
 XX
 XX 18-NOV-1999 (first entry)
 XX Mycobacterium tuberculosis ESAT-6 protein sequence.
 XX
 XX Mycobacterial; lactic acid bacterium; diagnosis; skin test; vaccine;
 XX delayed type hypersensitivity; DTH; ESAT-6 homodimer; tuberculosis;
 XX interferon-gamma release.
 XX
 XX Mycobacterium tuberculosis.
 XX
 XX WO9945119-A2.
 XX

PD 10-SEP-1999.
 XX 05-MAR-1999; 99WO-DK00109.
 XX 06-MAR-1998; 98DK-0000306.
 PR 06-MAR-1998; 98US-0077105.
 XX (STAT-) STATENS SERUM INST.
 XX Jensen CL, Folkersen J;
 PI WPI; 1999-551043/46.
 XX N-PSDB; AAZ21131.
 DR New mycobacterial polypeptide produced in lactic acid bacteria, useful
 PT in tuberculosis diagnosis and vaccines -
 XX Disclosure; Page 74; 76pp; English.
 XX The present invention describes a bioreactive polypeptide (or
 CC immunologically equivalent analogue) produced in lactic acid bacteria
 CC which reacts with lymphoid cells primed with Mycobacterium tuberculosis
 CC complex mycobacteria (M. tuberculosis, M. africanum or M. bovis). The
 CC polypeptide and ESAT-6 polypeptides are useful in compositions for
 CC diagnosis of and vaccination against tuberculosis caused by
 CC M. tuberculosis complex mycobacteria. The ESAT-6 polypeptide can be used
 CC to diagnose ongoing/previous sensitisation with these bacteria by
 CC detecting cytokine release when contacting blood samples with the
 CC polypeptide. The bioreactive polypeptide may be used in diagnostic
 CC compositions and vaccines for mycobacteria other than of the
 CC M. tuberculosis complex, e.g. M. avium which infects poultry and
 CC occasionally humans, M. leprae; they are especially useful when they do
 CC not react with lymphoid cells previously primed with M. tuberculosis
 CC complex mycobacteria, and so do not give rise to a diagnostic reaction
 CC in individuals infected with these bacteria. The polypeptides may also
 CC be used in in vitro diagnostic tests e.g. stimulation of interferon-gamma
 CC release from lymphocytes. The polypeptide has similar or higher
 CC bioreactivity as currently used tuberculin reagent in the standard
 CC delayed type hypersensitivity (DTH) skin test for tuberculosis, but may
 CC have greater specificity, being better able to discriminate between
 CC lymphoid cells primed from tuberculosis and from previous vaccination.
 CC The present sequence represents M. tuberculosis ESAT-6 used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 196 AA;
 Query Match 100.0%; Score 479; DB 20; Length 196;
 Best Local Similarity 100.0%; Pred. No. 8.8e-44;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQQWNEAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 Db 5 MTEQQWNEAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 64
 QY 61 TATELNALQNLARTISEAGQAMASTEIGNVTGMFA 95
 Db 65 TATELNALQNLARTISEAGQAMASTEIGNVTGMFA 99
 RESULT 8
 AA72943
 ID AA72943 standard; Protein; 403 AA.
 XX
 AC AA72943;
 XX 21-JAN-1999 (first entry)
 DT
 XX Mycobacterium tuberculosis antigen ESAT6-MPT59.
 DE
 XX Mycobacterium tuberculosis; antigen; vaccine; immunological;
 KW immunogen; infection.
 XX
 OS Mycobacterium tuberculosis.

XX WO9844119-A1.
 PN 08-OCT-1998.
 PD 01-APR-1998; 98WO-DK00132.
 XX 05-JAN-1998; 98US-0070488.
 PR 02-APR-1997; 97DK-0000376.
 PR 18-APR-1997; 97US-0044624.
 PR 10-NOV-1997; 97DK-0001277.
 XX (STAT-) STATENS SERUM INST.
 PA Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB;
 XX Rosenkrands I, Weldingh K;
 PI WPI; 1998-542705/46.
 DR
 XX New isolated mycobacteria polypeptides and nucleic acids - used for
 PT developing products for the diagnosis of or vaccination against
 PT mycobacterial infections, particularly tuberculosis
 XX Disclosure; Page 233-234; 163pp; English.
 XX The present sequence represents a Mycobacterium tuberculosis protein.
 CC Products from the present invention, which describes protein fragments
 CC and nucleic acid fragments derived from M. tuberculosis, can be used in
 CC the detection of and prevention of mycobacterial infections. In
 CC particular, the proteins and nucleic acids can be used for the diagnosis
 CC of or vaccination against tuberculosis caused by M. tuberculosis,
 CC M. africanum or M. bovis.
 XX
 SQ Sequence 403 AA;
 Query Match 100.0%; Score 479; DB 19; Length 403;
 Best Local Similarity 100.0%; Pred. No. 2.3e-43;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQQWNEAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
 Db 22 MTEQQWNEAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 81
 QY 61 TATELNALQNLARTISEAGQAMASTEIGNVTGMFA 95
 Db 82 TATELNALQNLARTISEAGQAMASTEIGNVTGMFA 116
 RESULT 9
 AA21963
 ID AA21963 standard; Protein; 403 AA.
 XX
 AC AA21963;
 XX 06-SEP-1999 (first entry)
 DT
 XX Amino acid sequence of antigen ESAT-6.
 DE
 XX Immunogenic; Mycobacterium tuberculosis; immune response; infection;
 KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
 KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
 KW CFP7B; CFP19; CFP27; CFP30A; RD1-ORF; CFP10A; CFP16; CFP19; CFP23;
 KW CFP25A; CFP30B; CFP7B.
 XX Mycobacterium tuberculosis.
 OS
 XX WO9924577-A1.
 PN 20-MAY-1999.
 PD 08-OCT-1998; 98WO-DK00438.
 PF 01-APR-1998; 98WO-DK00132.
 PR

PR 10-NOV-1997; 97DK-0001277.
 PR 05-JAN-1998; 98US-0070488.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 XX Andersen P, Skjot R;
 XX
 DR WPI; 1999-347282/29.
 XX
 PT New immunogenic fragment of Mycobacterium tuberculosis

XX
 XX Examples; Page 250-251; 265pp; English.
 XX
 CC The invention describes a substantially pure immunogenic polypeptide
 CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a
 CC protective immune response against infections by mycobacteria belonging
 CC to the tuberculosis complex. The invention provides a (1) fusion
 CC polypeptide comprising at least one polypeptide fragment (I) and at least
 CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
 CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
 CC different amino acid sequence from M. tuberculosis, and/or including a
 CC sequence which protects the first amino acid sequence from in vivo
 CC degradation or post-translational processing; (3) a nucleic acid fragment
 CC that encodes the above polypeptides. The polypeptides and nucleic acid
 CC are useful as pharmaceuticals for diagnosis of and as antigens for
 CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
 CC bovis. The polypeptides are also useful for diagnosing ongoing or
 CC previous sensitization in an animal with bacteria belonging to the
 CC tuberculosis complex. The invention also describes the use of CFP7A or
 CC CFP30A or a T-cell epitope of for the induction of a strong immune
 CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
 CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
 CC test; use of CFP27, CFP30A, RDI-ORF3, RDI-ORF5, MPT59-ESAT6,
 CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
 CC cell epitope of for the preparation of an immunological composition; and
 CC for the preparation of a subunit vaccine.
 XX
 SQ Sequence 403 AA;

Query Match 100.0%; Score 479; DB 20; Length 403;
 Best Local Similarity 100.0%; Pred. No. 2.3e-43;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAASATQGNVTSIHSLDEGKSLTKLAAGWGGSGSEAYQGVQKWD 60
 DB 22 MTEQOWNFAGIEAASATQGNVTSIHSLDEGKSLTKLAAGWGGSGSEAYQGVQKWD 81
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 DB 82 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 116

RESULT 10
 AA72942
 ID AAW72942 standard; Protein; 404 AA.
 XX
 AC AAW72942;
 XX
 DT 21-JAN-1999 (first entry)
 DE Mycobacterium tuberculosis antigen MPT59-ESAT6.
 XX Mycobacterium tuberculosis; antigen; vaccine; immunological;
 KW Mycobacterium tuberculosis; antigen; vaccine; immunological;
 XX Mycobacterium tuberculosis.
 OS
 XX WO9844119-A1.
 PN
 XX 08-OCT-1998.
 PD
 XX 01-APR-1998; 98WO-DK00132.
 PF
 XX

PR 05-JAN-1998; 98US-0070488.
 PR 02-APR-1997; 97DK-0000376.
 PR 18-APR-1997; 97US-0044624.
 PR 10-NOV-1997; 97DK-0001277.
 XX
 XX (STAT-) STATENS SERUM INST.
 XX
 XX Andersen P, Florio W, Nielsen R, Oettinger T, Rasmussen PB;
 PI Rosenkrands I, Weidinger K;
 XX
 DR WPI; 1998-542705/46.
 XX
 XX New isolated mycobacteria polypeptides and nucleic acids - used for
 XX developing products for the diagnosis of or vaccination against
 XX mycobacterial infections, particularly tuberculosis
 XX
 FS Disclosure; Page 232-233; 163pp; English.
 XX
 CC The present sequence represents a Mycobacterium tuberculosis protein.
 CC Products from the present invention, which describes protein fragments
 CC and nucleic acid fragments derived from M. tuberculosis, can be used in
 CC the detection of and prevention of mycobacterial infections. In
 CC particular, the proteins and nucleic acids can be used for the diagnosis
 CC of or vaccination against tuberculosis caused by M. tuberculosis,
 CC M. africanum or M. bovis.
 XX
 SQ Sequence 404 AA;
 Query Match 100.0%; Score 479; DB 19; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.3e-43;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAASATQGNVTSIHSLDEGKSLTKLAAGWGGSGSEAYQGVQKWD 60
 DB 310 MTEQOWNFAGIEAASATQGNVTSIHSLDEGKSLTKLAAGWGGSGSEAYQGVQKWD 369
 QY 61 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 95
 DB 370 TATELNALQNLARTISEAGQAMASTEAGNVTGMFA 404

RESULT 11
 AA721962
 ID AAY21962 standard; Protein; 404 AA.
 XX
 AC AAY21962;
 XX
 DT 06-SEP-1999 (first entry)
 DE Amino acid sequence of antigen MPT59.
 XX Immunogenic; Mycobacterium tuberculosis; immune response; infection;
 KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
 KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
 KW CFP7B; CFP19; CFP23; CFP30A; RDI-ORF; CFP10A; CFP16; CFP19; CFP23;
 KW CFP25A; CFP30B; CFP7B.
 XX Mycobacterium tuberculosis.
 OS
 XX WO9524577-A1.
 PN
 XX 20-MAY-1999.
 PD
 XX 08-OCT-1998; 98WO-DK00438.
 PF
 XX 01-APR-1998; 98WO-DK00132.
 PR 10-NOV-1997; 97DK-0001277.
 PR 05-JAN-1998; 98US-0070488.
 XX
 XX (STAT-) STATENS SERUM INST.
 XX Andersen P, Skjot R;
 XX

DE WPI; 1999-347282/29.

XX New immunogenic fragment of Mycobacterium tuberculosis

PS Examples; Page 249-250; 265pp; English.

XX The invention describes a substantially pure immunogenic polypeptide
 CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a
 CC protective immune response against infections by mycobacteria belonging
 CC to the tuberculosis complex. The invention provides a (1) fusion
 CC polypeptide comprising at least one polypeptide fragment (I) and at least
 CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
 CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
 CC different amino acid sequence from M. tuberculosis, and/or including a
 CC sequence which protects the first amino acid sequence from in vivo
 CC degradation or post-translational processing; (3) a nucleic acid fragment
 CC that encodes the above polypeptides. The polypeptides and nucleic acid
 CC are useful as pharmaceuticals, for diagnosis of and as antigens for
 CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
 CC bovis. The polypeptides are also useful for diagnosing ongoing or
 CC previous sensitization in an animal with bacteria belonging to the
 CC tuberculosis complex. The invention also describes the use of CFP7A or
 CC CFP30A or a T-cell epitope of for the induction of a strong immune
 CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
 CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
 CC test; use of CFP27, CFP30A, RD1-ORF2, RD1-ORF3, RD1-ORF5, MPT59-ESAT6,
 CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
 CC cell epitope of for the preparation of an immunological composition; and
 CC for the preparation of a subunit vaccine.

XX Sequence 404 AA;

Query Match 100.0%; Score 479; DB 20; Length 404;

Best Local Similarity 100.0%; Pred. No. 2.3e-43;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAYQGQKWD 60

Db 310 MTEQWNPAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAYQGQKWD 369

QY 61 TATELNNALQNLARTISEAGQAMASTEIGNVTGMFA 95

Db 370 TATELNNALQNLARTISEAGQAMASTEIGNVTGMFA 404

RESULT 12

AAW32466

ID AAW32466 standard; Protein; 51 AA.

XX AAW32466;

XX 09-JAN-1998 (first entry)

XX Mycobacterium tuberculosis antigen ESAT-6.

XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;

XX skin testing; M.tuberculosis.

XX Mycobacterium tuberculosis.

XX WO9709428-A2.

XX 13-MAR-1997.

XX 30-AUG-1996; 96WO-US14674.

XX 12-JUL-1996; 96US-0680574.

XX 01-SEP-1995; 95US-0523436.

XX 22-MAR-1995; 95US-0533634.

XX 22-MAR-1996; 96US-0620874.

XX 05-JUN-1996; 96US-0659683.

XX (CORI-) CORIXA CORP.

XX Campos-neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAW;

XX Twardzik DR, Vedvick TH;

XX WPI; 1997-192904/17.

XX N-PSDB; AAT91463.

XX New immunogenic polypeptide(s) from soluble M. tuberculosis antigens

XX - useful for diagnosis of M. tuberculosis infection

XX Claim 43; Page 147; 190pp; English.

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Campos-neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAW;

Twardzik DR, Vedvick TH;

WPI; 1997-192903/17.

N-PSDB; AAT91529.

New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are
 useful in vaccines for prevention or treatment of tuberculosis, also
 for diagnosis

Disclosure; Page 135; 168pp; English.

A new immunogenic polypeptide has been developed comprising an
 immunogenic part of a soluble Mycobacterium tuberculosis antigen (or
 its variant differing only in conservative substitutions and/or
 modifications). The present sequence represents a M.tuberculosis
 antigen, ESAT-6. The immunogenic protein, and fusion proteins
 containing one or more of the proteins or one of the proteins plus
 ESAT-6, are useful in vaccines, preferably when formulated with a
 non-specific adjuvant, to induce an immune response against
 M.tuberculosis (for treatment or prevention).

Sequence 51 AA;

Query Match 54.1%; Score 259; DB 18; Length 51;

Best Local Similarity 100.0%; Pred. No. 9.3e-21;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQWNPAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAY 51

Db 1 MTEQWNPAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAY 51

RESULT 13

AAW32339

ID AAW32339 standard; Protein; 51 AA.

XX AAW32339;

XX 13-JAN-1998 (first entry)

XX Mycobacterium tuberculosis antigen ESAT-6.

XX Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant;

XX skin testing; M.tuberculosis.

XX Mycobacterium tuberculosis.

XX WO9709429-A2.

XX 13-MAR-1997.

XX 30-AUG-1996; 96WO-US14675.

XX 12-JUL-1996; 96US-0680573.

XX 01-SEP-1995; 95US-0523435.

XX 22-MAR-1995; 95US-0532136.

XX 22-MAR-1996; 96US-0620280.

XX 05-JUN-1996; 96US-0658800.

XX (CORI-) CORIXA CORP.

XX Campos-neto A, Dillon DC, Houghton R, Reed SG, Skeiky YAW;

XX Twardzik DR, Vedvick TH;

XX WPI; 1997-192904/17.

XX N-PSDB; AAT91463.

New immunogenic polypeptide(s) from soluble M. tuberculosis antigens
 - useful for diagnosis of M. tuberculosis infection

Claim 43; Page 147; 190pp; English.

XX DE M. tuberculosis ESAT-6 amino acid sequence.
 XX
 KW Mycobacterium tuberculosis; M. tuberculosis; antigen; immunogen;
 KM immunotherapy; diagnosis; immunisation; vaccine; infection;
 KM immune response; skin test.
 XX
 CS Mycobacterium tuberculosis.
 XX
 PN WO9942076-A2.
 XX
 ED 26-AUG-1999.
 XX
 FF 17-FEB-1999; 99WO-US03268.
 XX
 XX 05-MAY-1998; 98US-0072967.
 PR 18-FEB-1998; 98US-0025197.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
 XX
 DR WPI: 1999-527409/44.
 DR N-PSDB; AAZ19303.
 XX
 PT New antigens from Mycobacterium tuberculosis useful in diagnostic
 PT skin tests and protective or therapeutic vaccines or compositions
 XX
 PS Disclosure; Page 120; 299pp; English.
 XX
 CC The present invention describes polypeptides comprising an immunogenic
 CC part of a Mycobacterium tuberculosis antigen (Ag). Also described
 CC are vaccines and fusion protein containing M. tuberculosis Ag's.
 CC M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and
 CC other polypeptides fragments, can be used in pharmaceutical compositions
 CC or vaccines to generate a protective or therapeutic immune response to
 CC M. tuberculosis and as reagents in skin tests for diagnosis of
 CC tuberculosis. Ag can induce proliferation of, or cytokine secretion
 CC by, T, B or natural killer cells and/or macrophages in
 CC tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAY39083 to
 CC AAY39225 are used in the exemplification of the present invention.
 XX
 SQ Sequence 51 AA;
 Query Match 54.1%; Score 259; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDGGKSLTKLAAAWGGSGSEAY 51
 DB 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDGGKSLTKLAAAWGGSGSEAY 51
 RESULT 17
 AAY38988
 ID AAY38988 standard; Protein; 51 AA.
 XX
 AC AAY38988;
 XX
 DT 05-NOV-1999 (first entry)
 XX
 XX M. tuberculosis recombinant antigen protein ESAT-6.
 DE
 XX Antigen; diagnosis; detection; infection; antibody; immunisation;
 KW vaccine; immunity.
 KW
 XX Mycobacterium tuberculosis.
 OS
 XX WO9942118-A2.
 PN
 XX 26-AUG-1999.
 PD
 XX

PF 17-FEB-1999; 99WO-US03265.
 XX
 PR 05-MAY-1998; 98US-0072596.
 PR 18-FEB-1998; 98US-0024753.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Campos-Neto A, Dillon DC, Hendrickson RC, Houghton R;
 PI Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
 XX
 DR WPI: 1999-527416/44.
 DR N-PSDB; AAZ19091.
 XX
 PT New polypeptide comprising antigenic portions of M. tuberculosis
 PS Claim 51; Page 165; 323pp; English.
 XX
 CC This invention describes novel recombinant antigens and their encoding
 CC nucleic acids derived from Mycobacterium tuberculosis. The novel
 CC polypeptides are useful for detecting M. tuberculosis infection in a
 CC biological sample by detecting antibodies which bind with the
 CC polypeptides, and are useful as vaccines for immunizing against
 CC M. tuberculosis infection. The new detection methods are needed as
 CC current vaccination strategies do not provide 100% immunity.
 XX
 SQ Sequence 51 AA;
 Query Match 54.1%; Score 259; DB 20; Length 51;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDGGKSLTKLAAAWGGSGSEAY 51
 DB 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDGGKSLTKLAAAWGGSGSEAY 51
 RESULT 18
 AAU01897
 ID AAU01897 standard; Protein; 51 AA.
 AC AAU01897;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Mycobacterium tuberculosis partial antigen ESAT-6.
 XX
 KW ESAT-6; antigen; vaccine; tuberculosis; AIDS;
 KW acquired immunodeficiency disease.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200124820-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-US28095.
 XX
 PR 07-OCT-1999; 99US-0158338.
 PR 07-OCT-1999; 99US-0158425.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 XX Skeiky Y, Reed S, Houghton RL, McNeill PD, Dillon DC, Lodes ML;
 PI
 DR WPI: 2001-290576/30.
 DR N-PSDB; AAS03787.
 XX
 XX Vaccinating against Mycobacteria infections in mammals using fusion
 PT proteins comprising combinations of heterologous antigens
 XX
 PS Disclosure; Page 164; 168pp; English.
 XX
 CC The sequence represents Mycobacterium tuberculosis ESAT-6 antigen.

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CC Compositions comprising at least 2 heterologous antigens, as a fusion
 CC protein, and vectors expressing the fusion proteins are used as vaccines
 CC to prophylactically immunise mammals (especially humans) against
 CC infection by Mycobacteria. The compositions contain at least 2
 CC heterologous antigens that increase the serological sensitivity of
 CC individuals infected with tuberculosis, a disease frequently affecting
 CC patients with acquired immunodeficiency disease, AIDS.
 XX
 SQ Sequence 51 AA;
 Query Match 54.1%; Score 259; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDDEKQSLTKLAAWGGSGSEAY 51
 DB 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDDEKQSLTKLAAWGGSGSEAY 51
 RESULT 19
 AAE29716
 ID AAE29716 standard; Protein; 51 AA.
 XX
 AC AAE29716;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis ESAT-6 antigenic protein.
 XX
 KW Vaccine; immunity; diagnostic agent; gene therapy; ESAT-6 antigen.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200272792-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 13-MAR-2002; 2002WO-US08223.
 XX
 PR 13-MAR-2001; 2001US-275837P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky Y, Brannon M, Guderian J;
 XX
 DR WPI; 2002-759844/82.
 DR N-PSDB; AAD29716.
 XX
 PT New recombinant nucleic acid molecule comprising a Leishmania TSA,
 PT Leif, M15 or 6H polynucleotide, useful as vaccine to elicit protective
 PT immunity against pathogenic microorganisms e.g. Leishmania and
 PT Mycobacterium tuberculosis
 XX
 PS Disclosure; Page 106; 155pp; English.
 CC The invention relates to a recombinant nucleic acid molecule encoding a
 CC fusion polypeptide. The recombinant nucleic acid comprises a heterologous
 CC polynucleotide sequence encoding an antigen or an antigenic fragment from
 CC Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a
 CC polypeptide or its fragment. The Leishmania polynucleotide is selected
 CC from TSA, Leif, M15, and 6H polynucleotides. Sequences of the invention
 CC are used in methods for eliciting immune response in mammals. They are
 CC useful as vaccines to elicit protective immunity against pathogenic
 CC microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion
 CC polypeptides are used for enhancing the expression of polynucleotides,
 CC as in vivo diagnostic agents and for raising antibodies in a non-human
 CC animal. The invention is used in gene therapy. The present sequence is
 CC M. tuberculosis ESAT-6 antigenic protein.
 XX
 SQ Sequence 51 AA;
 Query Match 54.1%; Score 259; DB 23; Length 51;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDDEKQSLTKLAAWGGSGSEAY 51
 DB 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDDEKQSLTKLAAWGGSGSEAY 51
 RESULT 20
 AAE17580
 ID AAE17580 standard; Protein; 51 AA.
 XX
 AC AAE17580;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Mycobacterium species ESAT-6 protein.
 XX
 KW Fusion protein; antigen; serological sensitivity; immune response;
 KW tuberculosis; infection; vaccine; ESAT-6 protein.
 XX
 OS Mycobacterium sp.
 XX
 PN WO200198460-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 20-JUN-2001; 2001WO-US19959.
 XX
 PR 20-JUN-2000; 2000US-0597796.
 PR 01-FEB-2001; 2001US-265737P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky Y, Reed S, Alderson M;
 XX
 DR WPI; 2002-147798/19.
 DR N-PSDB; AAD28351.
 XX
 PT Composition comprising Mtb39 antigen and Mtb32A antigen from
 PT Mycobacterium species, useful for eliciting immune response in a
 PT subject
 XX
 PS Claim 9; Page 122; 136pp; English.
 CC The present invention relates to fusion proteins containing at least
 CC two Mycobacterium species antigens, nucleotides encoding them and
 CC compositions comprising such fusion proteins. The present invention
 CC particularly relates to nucleic acids encoding fusion proteins that
 CC include two or more individual M. tuberculosis antigens which increase
 CC the serological sensitivity of sera from individuals infected with
 CC tuberculosis and methods for their use in diagnosis, prevention and
 CC treatment of tuberculosis infection. Sequences of the invention are
 CC useful for eliciting an immune response in a mammal, e.g., human,
 CC immunised with BCG. They are useful in the diagnosis, treatment and
 CC prevention of Mycobacterium infection. The fusion proteins and the
 CC polynucleotides are useful as diagnostic tools in patients infected
 CC with Mycobacterium, in vitro and in vivo assays for detecting humoral
 CC antibodies or cell-mediated immunity against M. tuberculosis, for the
 CC diagnosis of an infection or monitoring of disease progression, as
 CC immunogens to generate or elicit a protective immune response in a
 CC patient and for raising anti-M. tuberculosis antibodies in a non-human
 CC animal. Sequences of the invention are also used as vaccines. Mtb32A
 CC fusion proteins of the invention are useful as in vivo diagnostic agents
 CC for intradermal skin test. The present sequence is Mycobacterium species
 CC ESAT-6 protein.
 XX
 SQ Sequence 51 AA;
 Query Match 54.1%; Score 259; DB 23; Length 51;
 Best Local Similarity 100.0%; Pred. No. 9.3e-21;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDDEKQSLTKLAAWGGSGSEAY 51

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DB      1 MTEQWNEAGTEAAASAIQGNVTSIHSLDDEGKQSLTKLAANGSGSEAY 51
|||||
RESULT 21
ABU05360
ID      ABU05360 standard; Protein; 95 AA.
XX      AC
XX      AC ABU05360;
XX      DT
XX      DT 08-APR-2003 (first entry)
XX      DE
XX      DE M. tuberculosis and M. leprae marker protein #11.
XX      KW
XX      KW Mycobacterioses; survival; virulence; protective antigen; vaccine;
XX      KW mycobacterial disease; tuberculosis; leprosy.
XX      OS
XX      OS Mycobacterium tuberculosis.
XX      OS Mycobacterium leprae.
XX      PN
XX      PN W0200274903-A2.
XX      PD
XX      PD 26-SEP-2002.
XX      PF
XX      PF 22-FEB-2002; 2002WO-IB01973.
XX      PF
XX      PF 22-FEB-2001; 2001US-270123P.
XX      PE
XX      PE (INSP ) INST PASTEUR.
XX      PA
XX      PA Cole S;
XX      PI
XX      PI WPI; 2002-759885/82.
XX      DR
XX      DR
XX      PT
XX      PT Identifying and selecting genes for survival or virulence of
XX      PT Mycobacteria by a comparative genomic analysis of the sequences of
XX      PT Mycobacterium tuberculosis and M. leprae -
XX      PS
XX      PS Claim 17; Page 174; 874pp; English.
XX      CC
XX      CC This invention relates to a novel method for identifying essential genes
XX      CC for survival or virulence of mycobacteria species. The method comprises
XX      CC aligning the genomic sequence of a first mycobacterium species on a
XX      CC genomic sequence of a second mycobacterium species and selecting a
XX      CC polynucleotide sequence that is highly conserved in both genomes with no
XX      CC counterparts in other bacterial genomic sequences and that corresponds
XX      CC to an essential gene for the survival or virulence of mycobacterium
XX      CC species. The method of the invention is useful for detecting M.
XX      CC tuberculosis or M. leprae infection. The method reduces the number of
XX      CC potential new targets and protective antigens for new drugs and vaccine
XX      CC compositions to treat and prevent mycobacterial diseases, particularly
XX      CC tuberculosis and leprosy. The present sequence represents a marker
XX      CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
XX      CC identified using the method of the invention.
XX      SQ
XX      SQ Sequence 95 AA;
XX      Query Match 38.8%; Score 186; DB 23; Length 95;
XX      Best Local Similarity 36.3%; Pred. No. 1.7e-12;
XX      Matches 33; Conservative 27; Mismatches 31; Indels 0; Gaps 0;
XX      QY
XX      QY 4 QQWNEAGIEAASAIQGNVTSIHSLDEGKQSLTKLAANGSGSEAYQVQKWDATAT 63
XX      Db
XX      Db 3 QAWHFFALQGVNNEQSGRIDALLEQCOESLTKLQSSWHGSGNESYSVQRNFQNT 62
XX      QY
XX      QY 64 ELNNALQNLRITISEAGQAMASTEAGNVGMF 94
XX      Db
XX      Db 63 GINHALGDLVQALNHSAETVQTEAGVMSMF 93
XX      RESULT 22
XX      AAG90391
XX      ID AAG90391 standard; Protein; 96 AA.

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XX      AAG90391;
XX      DT
XX      DT 26-SEP-2001 (first entry)
XX      DE
XX      DE C glutamicum protein fragment SEQ ID NO: 4145.
XX      KW
XX      KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX      KW organic acid synthesis.
XX      OS
XX      OS Corynebacterium glutamicum.
XX      PN
XX      PN EP1108790-A2.
XX      PD
XX      PD 20-JUN-2001.
XX      PF
XX      PF 18-DEC-2000; 2000EP-0127688.
XX      PF
XX      PF 16-DEC-1999; 99JP-0377484.
XX      PF
XX      PF 07-APR-2000; 2000JP-0159162.
XX      PF
XX      PF 03-AUG-2000; 2000JP-0280988.
XX      PA
XX      PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX      PI
XX      PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX      PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX      DR
XX      DR WPI; 2001-376931/40.
XX      DR
XX      DR N-PSDB; AAH65610.
XX      PT
XX      PT Novel polynucleotides derived from Coryneform bacteria, for identifying
XX      PT mutation point of a gene, measuring expression of a gene, analysing
XX      PT expression profile or pattern of a gene and identifying homologous gene
XX      PS
XX      PS Claim 17; SEQ ID NO: 4145; 246pp + Sequence Listing; English.
XX      CC
XX      CC The present invention provides a number of nucleotide and protein
XX      CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX      CC are useful for identifying the mutation point of a gene derived from a
XX      CC mutant of coryneform bacterium, measuring expression amount and
XX      CC analysing the expression profile or expression pattern of a gene derived
XX      CC from Coryneform bacterium, and identifying a homologue of a gene derived
XX      CC from coryneform bacterium. Coryneform bacteria are useful for producing
XX      CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX      CC particularly L-lysine. The present sequence is a protein described
XX      CC in the exemplification of the invention.
XX      CC Note: The sequence data for this patent did not form part of the printed
XX      CC specification, but was obtained in electronic format directly from the
XX      CC European Patent Office.
XX      SQ
XX      SQ Sequence 96 AA;
XX      Query Match 31.5%; Score 151; DB 22; Length 96;
XX      Best Local Similarity 37.5%; Pred. No. 1.1e-08;
XX      Matches 30; Conservative 14; Mismatches 36; Indels 0; Gaps 0;
XX      QY
XX      QY 5 QWNEAGIEAASAIQGNVTSIHSLDEGKQSLTKLAANGSGSEAYQVQKWDATATE 64
XX      Db
XX      Db 5 RVEFGAIQGAADINSTSGRINSLDGLKSLQPMVASWESESEYSAQLKWDRAAE 64
XX      QY
XX      QY 65 LNNALQNLRITISEAGQAMA 84
XX      Db
XX      Db 65 LNTILATISNTVAQGAERMS 84
XX      RESULT 23
XX      AAW35547
XX      ID AAW35547 standard; peptide; 20 AA.
XX      AC
XX      AC AAW35547;
XX      DT
XX      DT 25-MAR-2003 (updated)

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DT 22-APR-1998 (first entry)
 XX ESAT-6 antigen SEQ ID NO:119 from WO9738011.
 XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.
 KW Synthetic.
 OS
 XX WO9738011-A1.
 XX 16-OCT-1997.
 XX 03-APR-1997; 97WO-DK00146.
 XX 03-APR-1996; 96DK-0000398.
 XX (PEPR-) PEPRESEARCH AS.
 XX Heegaard PMH, Jakobsen PH;
 XX WPI; 1997-512645/47.
 XX Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives
 XX
 PS Example 32; Page 156; 262pp; English.
 CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary, and
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC (A)-solid phase complex can be used as a scaffold for the production of
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an immunostimulating complex (iscom) resulting in
 CC (A)-iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 20 AA;
 Query Match 22.1%; Score 106; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 51 YGVGVQKWDATATELNALQ 70
 DB 1 YGVGVQKWDATATELNALQ 20
 RESULT 24
 AAY88580
 ID AAY88580 standard; peptide; 20 AA.
 XX
 AC AAY88580;
 XX
 DT 11-AUG-2000 (first entry)
 XX Antigenic C-terminal sequence of ESAT-6.
 DE
 XX

KW Ligand presenting assembly; early secreted antigen target 6; ESAT-6;
 KW bacteria; detect; diagnosis; allergen; cancer; vaccine; immune response;
 KW neurotropic factor; autoimmune-system related compound; LPA; fungi;
 KW parasite; cell-adhesion molecule.
 OS Mycobacterium tuberculosis.
 XX
 PH Key Location/Qualifiers
 FT Cross-links 20
 FT /note= "Gln at position 20 is linked via a linker to Gln
 FT at position 20 of an identical peptide, where
 FT the linker is COCH2-CH(NH-Lys)-CH2CO, and the
 FT Lys residue contained in the linker is also
 FT linked to another peptide (see AAY88579)."
 XX
 PN WO200018791-A1.
 XX
 XX 06-APR-2000.
 PD
 XX 29-SEP-1999; 99WO-DK00510.
 PF
 XX 29-SEP-1998; 98DK-0001233.
 PR
 XX (STAT-) STATENS SERUM INST.
 PA (HOLM/) HOLM A.
 PA
 XX Holm A, Jorgensen RM, Ostergaard S, Theisen M;
 PI WPI; 2000-303438/26.
 XX
 DR New ligand presenting assemblies useful for diagnosis, treatment and
 XX prevention of diseases caused by e.g. viruses, bacteria, toxins,
 PT allergens, autoimmune system-related compounds, cancer-related
 PT compounds, cell adhesion molecules
 XX
 PS Claim 34; Page 81; 100pp; English.
 CC This sequence represents an antigenic C-terminal sequence from the
 CC Mycobacterium tuberculosis early secreted antigenic target 6 (ESAT-6)
 CC protein. The peptide is presented on the new ligand presenting assembly
 CC of the invention. The invention relates to method for preparing ligand
 CC presenting assemblies (LPAs) comprising:
 CC (a) providing by solid phase synthesis, or fragment coupling, ligands
 CC comprising desired sequences (e.g. the present sequence), the ligands
 CC being attached to a solid phase;
 CC (b) if necessary, deprotecting any N-terminal amino groups while the
 CC ligands are still attached to the solid phase;
 CC (c) reacting the ligands having unprotected N-terminal amino groups with
 CC an achiral di-, tri- or tetracarboxylic acid, to provide a construct
 CC having a ring structure; and
 CC (d) cleaving the construct from the solid phase, to provide an LPA
 CC comprising ligands having free C-terminal groups. The LPAs can be used
 CC for raising an immune response in an animal. They can also be used in
 CC vaccines and for generating antibodies in an animal. Alternatively they
 CC can be used for the treatment, alleviation, detection, diagnosis, or
 CC prophylaxis of diseases caused by viruses, bacteria, toxins, allergens,
 CC autoimmune system-related compounds, cancer related compounds, cell
 CC adhesion molecules, neurotropic factors, fungi or parasites. Use of the
 CC method enables the preparation of very long ring systems interconnected
 CC by reaction with the achiral di-, tri- or tetracarboxylic acid. The ring
 CC structure formed between desired sequences further enables additional
 CC presentation of desired sequences and chemical moieties. The LPAs provide
 CC very flexible systems for polyfunctional constructs, and furthermore,
 CC products of high purity are obtained.
 XX
 SQ Sequence 20 AA;
 Query Match 22.1%; Score 106; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.7e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 YGVGVQKWDATATELNALQ 70
 |||||||||||||||||||||


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Db      1 YQGVQKWDATATLNNALQ 20

RESULT 25
AAE12275
ID AAE12275 standard; peptide; 20 AA.
XX
AC AAE12275;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mycobacterium tuberculosis (Mtb) peptide #60.
XX
KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
KW infection; anti-Mtb immune response.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200170774-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US08906.
XX
PR 20-MAR-2000; 2000US-190834P.
XX
PA (UYBR-) UNIV BROWN RES FOUND.
XX
PI Degroot AS;
XX
DE WPI; 2001-616401/71.
XX
PT New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis -
XX
PS Disclosure; Fig 4; 42pp; English.
XX
CC The present invention relates to Mycobacterium tuberculosis (Mtb)
CC vaccine candidate peptides. The invention also relates to a method
CC for identifying Mtb vaccine candidate peptides as well as vaccines
CC comprising these candidate peptides. Vaccines of the invention and
CC Mtb vaccine candidate peptides are useful for inducing an anti-
CC Mycobacterium tuberculosis (anti-Mtb) immune response by raising
CC anti-Mtb antibody in a mammalian subject preferably human. They
CC are used for immunising a mammalian subject, preferably humans,
CC against infection caused by Mycobacterium tuberculosis. The present
CC sequence is a Mtb vaccine candidate peptide.
XX
SQ Sequence 20 AA;
XX
Query Match 21.1%; Score 101; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QWNFAGIEAASAIQGNVTS 24
|||||
Db 1 QWNFAGIEAASAIQGNVTS 20

RESULT 26
AAE12277
ID AAE12277 standard; peptide; 20 AA.
XX
AC AAE12277;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mycobacterium tuberculosis (Mtb) peptide #62.
XX
KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
KW infection; anti-Mtb immune response.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200170774-A2.
XX
PD 27-SEP-2001.
XX
PF 20-MAR-2001; 2001WO-US08906.
XX
PR 20-MAR-2000; 2000US-190834P.
XX
PA (UYBR-) UNIV BROWN RES FOUND.
XX
PI Degroot AS;
XX
DE WPI; 2001-616401/71.
XX
PT New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis -
XX
PS Disclosure; Fig 4; 42pp; English.
XX
CC The present invention relates to Mycobacterium tuberculosis (Mtb)
CC vaccine candidate peptides. The invention also relates to a method
CC for identifying Mtb vaccine candidate peptides as well as vaccines
CC comprising these candidate peptides. Vaccines of the invention and
CC Mtb vaccine candidate peptides are useful for inducing an anti-
CC Mycobacterium tuberculosis (anti-Mtb) immune response by raising
CC anti-Mtb antibody in a mammalian subject preferably human. They
CC are used for immunising a mammalian subject, preferably humans,
CC against infection caused by Mycobacterium tuberculosis. The present
CC sequence is a Mtb vaccine candidate peptide.
XX
SQ Sequence 20 AA;
XX
Query Match 20.5%; Score 98; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 IQGNVTSIHSLDEGKQSLT 37
|||||
Db 1 IQGNVTSIHSLDEGKQSLT 20

RESULT 27
AAV21964
ID AAV21964 standard; Protein; 96 AA.
XX
AC AAV21964;
XX
DT 06-SEP-1999 (first entry)
XX
DE Amino acid sequence of antigen ORF7-1.
XX
KW Immunogenic; Mycobacterium tuberculosis; immune response; infection;
KW tuberculosis; fusion polypeptide; T-cell epitope; ESAT-6; MPT59; TB;
KW pharmaceutical; vaccination; M. africanum; M. bovis; CFP7A; CFP30A;
KW CFP7B; CFP19; CFP27; CFP30A; RDI-ORF; CFP10A; CFP16; CFP19; CFP23;
KW CFP25A; CFP30B; CFP7B.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9924577-A1.
XX
PD 20-MAY-1999.
XX
PF 08-OCT-1998; 98WO-DK00438.
XX
PR 01-APR-1998; 98WO-DK00132.
PR 10-NOV-1997; 97DK-0001277.
PR 05-JAN-1998; 98US-0070486.
XX
PA (STAT-) STATENS SERUM INST.
XX
PI Andersen P, Skjot R;

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XX WPI; 1999-347282/29.
DR N-PSDB; AAX81111.
XX
XX New immunogenic fragment of Mycobacterium tuberculosis
PT
XX
XX Claim 1; Page 252; 265pp; English.
XX
XX The invention describes a substantially pure immunogenic polypeptide
CC fragment (I) from Mycobacterium tuberculosis that is able to evoke a
CC protective immune response against infections by mycobacteria belonging
CC to the tuberculosis complex. The invention provides a (1) fusion
CC polypeptide comprising at least one polypeptide fragment (I) and at least
CC one fusion partner; (2) a fusion polypeptide fragment comprising a T-cell
CC epitope from M. tuberculosis protein ESAT-6, or MPT59 and a second
CC different amino acid sequence from M. tuberculosis, and/or including a
CC sequence which protects the first amino acid sequence from in vivo
CC degradation or post-translational processing; (3) a nucleic acid fragment
CC that encodes the above polypeptides. The polypeptides and nucleic acid
CC are useful as pharmaceuticals, for diagnosis of and as antigens for
CC vaccination against TB caused by Mycobacterium tuberculosis, africanum or
CC bovis. The polypeptides are also useful for diagnosing ongoing or
CC previous sensitization in an animal with bacteria belonging to the
CC tuberculosis complex. The invention also describes the use of CFP7A or
CC CFP30A or a T-cell epitope of for the induction of a strong immune
CC response in a mammal; use of CFP7B, CFP19 or MPT59-ESAT6 or a T-cell
CC epitope of for diagnosis of TB in a mammal by performing a DTH type skin
CC test; use of CFP27, CFP30A, RDI-ORF3, RDI-ORF5, MPT59-ESAT6,
CC ESAT6-MPT59, CFP10A, CFP16, CFP19, CFP23, CFP25A, CFP30B, CFP7B or a T-
CC cell epitope of for the preparation of an immunological composition; and
CC for the preparation of a subunit vaccine.
XX
XX Sequence 96 AA;
SQ
    Query Match      20.5%; Score 98; DB 20; Length 96;
    Best Local Similarity 30.2%; Pred. No. 0.0057;
    Matches 29; Conservative 16; Mismatches 39; Indels 12; Gaps 3;

QY 1 MTEQQWVFAGIEAASAIQGNVTSIHSLDEGKQSLTKIAAAGGSGSEAYGVQVKQDA 60
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSQIYVYFAMAHAGDMAGYAGTQLQSLQADIAEQAVLSSAQWGDGTGYQGWQW-- 58
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 61 TATELNNALONLARTISEAQWAST-EGNVGTGMEA 95
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 -----NQALEDLVR-----AYQSMGTHESNTMAMLA 85
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 28
AAE12276
XX ID AAE12276 standard; peptide; 20 AA.
XX AC AAE12276;
XX DT 18-DEC-2001 (first entry)
XX DE Mycobacterium tuberculosis (Mtb) peptide #61.
XX KW Mycobacterium tuberculosis; Mtb peptide; antibacterial; vaccine;
XX KW infection; anti-Mtb immune response.
XX OS Mycobacterium tuberculosis.
XX PN WO200170774-A2.
XX PD 27-SEP-2001.
XX PF 20-MAR-2001; 2001WO-US08906.
XX PR 20-MAR-2000; 2000US-190834P.
XX PA (UYBR-) UNIV BROWN RES FOUND.
XX PI Degroot AS;

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XX WPI; 2001-616401/71.
DR
XX New vaccine for immunizing a mammalian subject, preferably humans,
PT against infection caused by Mycobacterium tuberculosis
XX
XX Disclosure; Fig 4; 42pp; English.
XX
XX The present invention relates to Mycobacterium tuberculosis (Mtb)
CC vaccine candidate peptides. The invention also relates to a method
CC for identifying Mtb vaccine candidate peptides as well as vaccines
CC comprising these candidate peptides. Vaccines of the invention and
CC Mtb vaccine candidate peptides are useful for inducing an anti-
CC Mycobacterium tuberculosis (anti-Mtb) immune response by raising
CC anti-Mtb antibody in a mammalian subject, preferably human. They
CC are used for immunising a mammalian subject, preferably humans,
CC against infection caused by Mycobacterium tuberculosis. The present
CC sequence is a Mtb vaccine candidate peptide.
XX
XX Sequence 20 AA;
SQ
    Query Match      20.3%; Score 97; DB 22; Length 20;
    Best Local Similarity 100.0%; Pred. No. 0.00091;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAASAIQGNVTSIH 26
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 NFAGIEAASAIQGNVTSIH 20
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 29
AAW35548
XX ID AAW35548 standard; peptide; 19 AA.
XX AC AAW35548;
XX DT 25-MAR-2003 (updated)
XX DT 22-APR-1998 (first entry)
XX DE ESAT-6 antigen SEQ ID NO:120 from WO9738011.
XX KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
XX KW scaffold; inhibition; metastasis; wound healing; solid phase.
XX OS Synthetic.
XX PN WO9738011-A1.
XX PD 16-CCT-1997.
XX PF 03-APR-1997; 97WO-DK00146.
XX PR 03-APR-1996; 96DK-0000398.
XX PA (PEPR-) PEPRESEARCH AS.
XX PI Heegaard PMH, Jakobsen PH;
XX DR WPI; 1997-512645/47.
XX
XX Non-dendritic peptide carrier linked to a solid phase - useful as a
PT diagnostic agent and as a scaffold for production of chemical
PT derivatives
XX
XX Example 32; Page 156; 262pp; English.
XX
XX A non-dendritic peptide carrier (A) has been developed which is coupled
CC through a linker to a solid phase, forming a complex of (A)-solid phase.
CC Where (A) comprises 10-50 amino acids capable of forming a secondary
CC structure in a benign buffer after liberation from the solid phase, and
CC further the (A)-solid phase complex comprises an immunogenic substance
CC and/or an immune mediator coupled on (A). The present sequence
CC represents a peptide used in an example from the present invention. An

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PS Claim 34; Page 81; 100pp; English.

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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:35:17 : Search time 6.3333 Seconds
(without alignments)
1442.530 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQWNFAGIEAASALQG.....ISEAGQMASTEGNVTGMFA 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283102

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : PIR 76:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	479	100.0	95	2 A70803	early secretory an
2	186	38.8	95	2 T10031	early secretory an
3	96	20.0	96	2 F70857	hypothetical prote
4	86.5	18.1	100	2 B70977	hypothetical prote
5	85	17.7	96	2 F70836	hypothetical prote
6	81	16.9	96	2 H87225	hypothetical prote
7	80.5	16.8	90	2 A70600	probable cell suri
8	80	16.7	498	1 FLEC	hypothetical prote
9	79	16.5	104	2 C86954	flagellin - Escher
10	77.5	16.2	125	2 C70977	probable secreted
11	76	15.9	1037	2 D91045	hypothetical prote
12	75	15.7	490	2 H83286	aminoglycoside eff
13	75	15.7	1037	2 E65022	probable chemotaxi
14	75	15.7	1037	2 G85889	acridin resista
15	73.5	15.3	371	2 G96937	hypothetical prote
16	73	15.2	1204	2 B83566	cell wall-associat
17	72.5	15.1	238	2 T05959	probable bacteriop
18	72.5	15.1	756	2 A43582	1,3-beta-glucanase
19	72	15.0	96	2 D83771	surface antigen ms
20	72	15.0	637	2 C87322	hypothetical prote
21	72	15.0	1225	2 F75605	methyl-accepting c
22	72	15.0	1697	2 T00079	minor tail protein
23	72	15.0	6713	2 B89921	hypothetical prote
24	71.5	14.9	94	2 D70608	hypothetical prote
25	71.5	14.9	526	2 D75391	AlpG-related prote
26	71.5	14.9	927	2 A61739	transmembrane prot
27	71	14.8	97	2 H96904	uncharacterized sm
28	71	14.8	356	2 S02017	regulatory protein
29	70.5	14.7	94	2 B70930	hypothetical prote

30	70.5	14.7	94	2 C70662	hypothetical prote
31	70.5	14.7	94	2 D70560	hypothetical prote
32	70.5	14.7	388	2 A46173	Mip4 protein - Str
33	70.5	14.7	656	2 A72428	methyl-accepting c
34	70.5	14.7	656	2 E72379	methyl-accepting c
35	70.5	14.7	661	2 G72316	methyl-accepting c
36	70.5	14.7	1510	2 T13634	probable minor tai
37	70.5	14.7	2073	2 T43311	fatty acyl-CoA syn
38	70.5	14.7	2073	2 T39207	fatty acid synthas
39	70.5	14.7	2475	2 T00047	gellan lyase (EC 4
40	70	14.6	103	2 B70600	hypothetical prote
41	70	14.6	649	2 T45102	H+-transporting tw
42	70	14.6	710	1 S1283	hepatocyte growth
43	69.5	14.5	382	2 S15578	ipac protein - Shi
44	69.5	14.5	1509	2 B89985	hypothetical prote
45	69	14.4	572	2 C96024	probable glycerone
46	69	14.4	1037	2 A80816	probable efflux pu
47	68.5	14.3	103	2 T10920	3C3.11 protein - S
48	68	14.2	164	2 A45512	cold-regulated pro
49	68	14.2	335	2 T02211	1,3-beta-glucanase
50	68	14.2	388	2 S52536	fcra 15 protein -
51	68	14.2	405	2 A33939	Fc gamma (IgG) rec
52	68	14.2	409	2 S10485	licheninase (EC 3.
53	68	14.2	701	2 UC7184	gamma adducin - hu
54	67.5	14.1	238	2 T05962	flagellin - Shigel
55	67.5	14.1	364	2 S78461	phosphoglycerate m
56	67.5	14.1	395	2 D83782	hypothetical prote
57	67.5	14.1	495	2 S60175	aspartate aminotra
58	67.5	14.1	524	2 S44982	regulatory protein
59	67	14.0	231	2 A51503	flagellin - Shigel
60	67	14.0	293	2 D96560	phosphoglycerate m
61	67	14.0	451	2 B70805	hypothetical prote
62	67	14.0	550	2 S44980	hypothetical prote
63	67	14.0	562	2 D85439	tubulin-like prote
64	67	14.0	565	2 T41061	flagellin - Escher
65	67	14.0	1063	2 A40253	acidic nuclear pro
66	67	14.0	1738	1 A24558	complement C4 prec
67	67	14.0	2094	2 S33124	tpc protein - huma
68	67	14.0	3635	2 T10053	laminin alpha 5 ch
69	66.5	13.9	288	2 A99305	hypothetical prote
70	66.5	13.9	428	1 D71155	probable methyl-ac
71	66.5	13.9	454	2 A41659	benzoate 1,2-dioxy
72	66.5	13.9	457	2 G82925	hypothetical prote
73	66.5	13.9	595	2 B48658	hypothetical prote
74	66.5	13.9	74	2 G69371	flagellin - Escher
75	66.5	13.9	706	2 F82148	acetyl-CoA synthet
76	66.5	13.9	709	2 S75212	methyl-accepting c
77	66.5	13.9	1819	2 D97132	comE protein - Syn
78	66	13.8	424	2 S72695	uncharacterized ph
79	66	13.8	455	2 JC7550	L-aspartate oxidas
80	66	13.8	527	2 D87062	glucokinase (EC 2.
81	66	13.8	530	2 S62439	L-aspartate oxidas
82	66	13.8	626	2 F85295	hypothetical prote
83	66	13.8	627	2 T05789	hypothetical prote
84	66	13.8	927	2 AH1369	transmembrane prot
85	66	13.8	1467	2 A75564	conserved hypotet
86	65.5	13.7	137	2 JH0127	mobB protein - Esc
87	65.5	13.7	465	2 C43357	triacylglycerol li
88	65.5	13.7	531	2 D83297	probable chemotaxi
89	65.5	13.7	585	2 F90961	flagellin importe
90	65.5	13.7	585	2 F85809	hypothetical prote

ALIGNMENTS

RESULT 1

A70803
early secretory antigen target esat6 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence.revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70803; S49174
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70803

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-95 <COL>

A:Cross-references: GB:AL021220; GB:AL123456; NID:g3261558; PIDN:CAA17967.1; PID:el26412

A:Experimental source: strain H37RV

R:Soerensen, A.L.; Nagai, S.; Houn, G.; Andersen, P.; Andersen, A.B. submitted to the EMBL Data Library, June 1994

A:Reference number: S49174

A:Accession: S49174

A:Molecule type: DNA

A:Residues: 1-13, 'R', 15-22, 'S', 24-95 <SOE>

A:Cross-references: EMBL:X79562; NID:g531708

C:Genetics:

A:Gene: csat6

Query Match 100.0%; Score 479; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.3e-39;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAWGGSGSEAYQGVQKWDA 60
|||
DB 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAWGGSGSEAYQGVQKWDA 60

QY 61 TATELNALQNARTISEAGQAMASTEGNVTGMFA 95
|||
DB 61 TATELNALQNARTISEAGQAMASTEGNVTGMFA 95

RESULT 2
T10031
early secretory antigen target 6 protein homolog - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C:Accession: T10031
R:Eiglmeyer, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T. Mol. Microbiol. 7, 197-206, 1993
A:Title: Use of an ordered cosmid library to deduce the genomic organization of Mycobact
A:Reference number: Z16917; MUID:93188700; PMID:8446027
A:Accession: T10031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-95 <EIG>
A:Cross-references: EMBL:Y14967; NID:g2370268; PIDN:CAA75200.1; PID:g2370279
C:Genetics:
A:Gene: esx

Query Match 38.8%; Score 186; DB 2; Length 95;
Best Local Similarity 36.3%; Pred. No. 3.3e-11;
Matches 33; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

QY 4 QQWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAWGGSGSEAYQGVQKWDA 63
|||
DB 3 QAWHFPALQAVNELQGSQSRIDALLEQCESLTKLQSSWHGSGNESYSVQRNFQNT 62

QY 64 ELNNALQNARTISEAGQAMASTEGNVTGMF 94
|||
DB 63 GINHALGDLVQAINHSAFTMQTEAGVMSMF 93

RESULT 3
F70857
hypothetical protein Rv3019c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70857
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70857

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-96 <COL>

A:Cross-references: GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CAA16104.1; PID:el23777

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv3019c

Query Match 20.0%; Score 96; DB 2; Length 96;
Best Local Similarity 30.2%; Pred. No. 0.018;
Matches 29; Conservative 16; Mismatches 39; Indels 12; Gaps 3;

QY 1 MTEQQWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAWGGSGSEAYQGVQKWDA 60
|||
DB 1 MSQIMYNYPAMMAHAGDWAGYAGTQSLCADIASQAVLSAWQGDGTGTYQGWQTOW-- 58

QY 61 TATELNALQNARTISEAGQAMASTEGNVTGMFA 95
|||
DB 59 -----NOALEDLVR-----AYQSMGTHESNTMAMLA 85

RESULT 4
B70977
hypothetical protein Rv3444c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: B70977
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: B70977

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-100 <COL>

A:Cross-references: GB:Z95389; GB:AL123456; NID:g3242261; PIDN:CAB08674.1; PID:e316051

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv3444c

Query Match 18.1%; Score 86.5; DB 2; Length 100;
Best Local Similarity 24.2%; Pred. No. 0.15;
Matches 22; Conservative 13; Mismatches 55; Indels 1; Gaps 1;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAWGGSGSEAYQGVQKWDA 64
|||
DB 9 YNFDALEYSVRQEIHTTAARFNAALQELRSQAPLQQLWTREAAAAYHAFQLKWHQAASA 68

QY 65 LNNAALQNARTISEAGQAMASTEGNVTGMFA 95
|||
DB 69 LNEILLDLGNVVRHGADDDVAHADRRRAAGAWA 99

RESULT 5
F70836
hypothetical protein Rv0288 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70836
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70836
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-96 <COL>
A:Cross-references: GB:AL021930; GB:AL123456; NID:g3261524; PIDN:CAA17363.1; PID:e125247
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: RV0288

Query Match 17.7%; Score 85; DB 2; Length 96;
Best Local Similarity 29.2%; Pred. No. 0.21;
Matches 28; Conservative 14; Mismatches 42; Indels 12; Gaps 3;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDA 60
DB 1 MSQIMYNYPAMLGHAGDMAGYAGTQLQSLGAEIAVEQAALQSAWQGDGTGTYQAWQAQW-- 58
QY 61 TATELNALONLARTISEAGQAMAST-EGNVVTGMFA 95
DB 59 -----NQAMEDLVR-----AYHAMSSTHEANTWAMMA 85

RESULT 6
H87225
probable cell surface protein [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
A:Accession: H87225
R:Colle, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, R.; Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.; Nature 409, 1007-1011, 2001
A:Title: Massive gene decay in the leprosy bacillus
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H87225
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-36 <STO>
A:Cross-references: GB:AL450380; NID:gl3093793; PIDN:CAC32062.1; GSPDN:GN00147
C:Genetics:
A:Gene: ML2531

Query Match 16.9%; Score 81; DB 2; Length 96;
Best Local Similarity 26.0%; Pred. No. 0.5;
Matches 26; Conservative 12; Mismatches 36; Indels 26; Gaps 3;

QY 1 MTEQOWNF-----AGTEAASAIQGNVTSIHSLLDEGKQSLTKLAAWGGSGSEAYQGV 53
DB 1 MTQIMYNYPAMLGHAGDMAGYAGTQLQSLGAEIAVEQAALQSAWQGDGTGTYQAWQAQW-- 58
QY 54 VQKQWDAATATL-----NNALONLARTISEAGQ 81
DB 54 WQVQWQATHEMVRAYHAMANTHONVTLAMLTROQAEAAK 93

RESULT 7
A70600
hypothetical protein Rv3904c - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: A70600
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70600

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <COL>
A:Cross-references: GB:Z94121; GB:AL123456; NID:g3261736; PIDN:CAB08097.1; PID:e3112273;
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: RV3904c

Query Match 16.8%; Score 80.5; DB 2; Length 90;
Best Local Similarity 31.0%; Pred. No. 0.52;
Matches 22; Conservative 10; Mismatches 32; Indels 7; Gaps 2;

QY 25 IHSLLDEGKQSLTKLAAWGGSGSEAYQGVQKQWDAATATLNALONLARTISEAGQAMA 84
DB 20 VEELVAETESLVTRLHVTWTGEGAAAHAEQAQRHWAAGEAMMQALAAQL-----TAAGQ---- 72
QY 85 STEGNNVTGMFA 95
DB 73 SAHANYTGAMA 83

RESULT 8
FLEC
flagellin - Escherichia coli (strain K-12)
C:Species: Escherichia coli
A:Variety: strain K-12
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Mar-2002
A:Accession: A37249; JVO0018; I41270; H64955; A28187
R:Kuwajima, G.; Asaka, J.I.; Fujiwara, T.; Fujiwara, T.; Node, K.; Kondo, E.
J. Bacteriol. 168, 1479-1483, 1986
A:Title: Nucleotide sequence of the hag gene encoding flagellin of Escherichia coli.
A:Reference number: A37249; MUID:87057066; PMID:3536885
A:Accession: A37249
A:Molecule type: DNA
A:Residues: 1-498 <KUN>
A:Cross-references: GB:MI4358; NID:gl46311; PIDN:AAA23950.1; PID:gl46312
A:Experimental source: strain K-12
R:Hananafusa, T.; Sakai, A.; Tomimaga, A.; Enomoto, M.
Mol. Gen. Genet. 216, 44-50, 1989
A:Title: Isolation and characterization of Escherichia coli hag operator mutants whose
A:Reference number: JVO0018; MUID:89281489; PMID:2659972
A:Accession: JVO0018
A:Molecule type: DNA
A:Residues: 1-284, 'L', 286-498 <HAN>
A:Cross-references: GB:X17440; NID:gl41649; PIDN:CAA35488.1; PID:g41651
A:Experimental source: strain K-12
R:Stakely, E.; Simon, M.
J. Bacteriol. 155, 74-81, 1983
A:Title: DNA sequence adjacent to flagellar genes and evolution of flagellar- phase vari
A:Reference number: I41269; MUID:83238225; PMID:6305924
A:Accession: I41270
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: GB:J01607; NID:gl46315; PIDN:AAA92491.1; PID:gl46317
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64955
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-498 <BLAT>
A:Cross-references: GB:AE0000285; GB:U00096; NID:gl788229; PIDN:AAC74990.1; PID:gl788232;
A:Experimental source: strain K-12, substrain MG1655
R:Kuwajima, G.
J. Bacteriol. 170, 3305-3309, 1988
A:Title: Construction of a minimum-size functional flagellin of Escherichia coli.
A:Reference number: A28187; MUID:88257060; PMID:3290204
A:Accession: A28187
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA

A;Residues: 1-15,140-402,489-498 <KU2>
A;Cross-references: GB:M21445; NID:G146313; PIDN:AAA23951.1; PID:G146314
C;Comment: This is the principal protein component of the flagellar filament, which is a
C;Genetics:
A;Gene: fliC; hag
A;Map position: 42 min
C;Superfamily: flagellin
C;Keywords: flagellum

Query Match 16.7%; Score 80; DB 1; Length 498;
Best Local Similarity 30.4%; Pred. No. 4.3;
Matches 24; Conservative 9; Mismatches 38; Indels 8; Gaps 1;

QY 9 AGIEAASAIQGNVTSIHSLDEGKQSLTKLAAANGSGSEAYQGVQKWDATATLNA 68
DB 394 AGGEALTAVANGKTTDLKALDDATASVDKFRSLG-----AVONRLDSAVTNLNT 445
QY 69 LONLARTISEAQMASTE 87
DB 446 TTNLSEAQRIQDADYATE 464

RESULT 9
C86954
probable secreted protein [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C86954
R;Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
ean, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C86954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104 <STO>
A;Cross-references: GB:AL450380; NID:G13092644; PIDN:CAC29871.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML0363

Query Match 16.5%; Score 79; DB 2; Length 104;
Best Local Similarity 25.8%; Pred. No. 0.86;
Matches 24; Conservative 14; Mismatches 50; Indels 6; Gaps 1;

QY 2 TEQWNFAGTEAASAIQGNVTSIHSLDEGKQSLTKLAAANGSGSEAYQGVQKWDAT 61
DB 16 TKSNTPLAGKSTARPA-----RFNALELRSQIAPLQQRWTRAAVVVPVQLKWHQA 69
QY 62 ATELNALQNLARTISEAQMASTEIGNVTGMPA 95
DB 70 ATALNEILDGNVIRAGAEVANTDRSGGVNA 103

RESULT 10
C70977
hypothetical protein Rv3445c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70977
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70977
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <COL>

A;Cross-references: GB:Z95389; GB:AL123456; NID:G3242261; PIDN:CAE08675.1; PID:e316052
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV3445c

Query Match 16.2%; Score 77.5; DB 2; Length 125;
Best Local Similarity 35.3%; Pred. No. 1.5;
Matches 18; Conservative 8; Mismatches 18; Indels 7; Gaps 1;

QY 41 AAWGGSEAYQGVQKWDATATLNNALQNLARTI-----SEAGAMA 84
DB 65 SWYGGAAARFQDVVDWRNAESTRLYHVLHATATIRNEAALRAGQIHA 115

RESULT 11
D91045
aminoglycoside efflux pump [imported] - Escherichia coli (strain O157:H7, substrain RIM
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: D91045
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1037 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36755.1; PID:G13362802; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC83332
C;Superfamily: acriflavin resistance protein

Query Match 15.9%; Score 76; DB 2; Length 1037;
Best Local Similarity 26.2%; Pred. No. 25;
Matches 27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;

QY 7 NFAGTFA-----AASAIQGNVTSIHSL-----DEGKQSLTKLAAANGSGSEAYQ 53
DB 48 NYPGSAQTLENTVTQVIEQNTMTGLDNLMTMSSQSGTQASVT-LSFKAGTDPDEAVQQ 106
QY 54 VQKWDATATLNNALQNLARTISEAQ-----AMASTEIGNV 90
DB 107 VQNLQSAKMKLPQAVQNGQLTVRKTGDTNLTIAFVSTDGSM 149

RESULT 12
H83286
probable chemotaxis transducer PA2867 [imported] - Pseudomonas aeruginosa (strain PA01
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83286
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83286
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <STO>
A;Cross-references: GB:AE004713; GB:AE004091; NID:G9948952; PIDN:AAG06255.1; GSPDB:GN0
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2867

Query Match 15.7%; Score 75; DB 2; Length 490;
Best Local Similarity 29.1%; Pred. No. 13;
Matches 23; Conservative 12; Mismatches 36; Indels 8; Gaps 2;


```
QY      8  PAGTEAASAIQGNVTSIHSLDEGKSLTKLAARWGGSGSEAYQGVQKWDATATELNN 67
Db      201 FNAWQAGYQRIIVGTVAATAATKLDGAQALARM-----GQVRQGMGLGQSQSETDTQTATATN- 255

QY      68 ALQNLARTISEAGQAMAST 86
Db      256 ---EMSTVFHIAQHAUT 271

RESULT 13
E65022
A:Title: acriflavin resistance protein acrD - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: E65022; C42959; S26997
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65022
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1037 <BLAT>
A:Cross-references: GB:AE000334; GB:U00096; NID:g1788813; PIDN:AACT5523.1; PID:g1788814;
A:Experimental source: strain K-12, substrain MGL655
R:Bouvier, J.; Richaud, C.; Higgins, W.; Bogler, O.; Stragier, P.
J. Bacteriol. 174, 5265-5271, 1992
A:Title: Cloning, characterization, and expression of the dapE gene of Escherichia coli.
A:Reference number: A42959; MUID:92355499; PMID:1644752
A:Accession: C42959
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 998-1037 <BOU>
A:Cross-references: GB:X57403; GB:S41761; NID:g41231; PIDN:CAA40663.1; PID:g41232
A:Note: sequence extracted from NCBI backbone (NCBIN:110333, NCBI:P:110334)
R:Stragier, P.
submitted to the EMBL Data Library, January 1991
A:Reference number: S26997
A:Accession: S26997
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 998-1037 <STP>
A:Cross-references: EMBL:X57403; NID:g41231; PIDN:CAA40663.1; PID:g41232
A:Experimental source: strain K-12
C:Genetics:
A:Gene: acrD
C:Superfamily: acriflavin resistance protein
F:14-30/Domain: transmembrane #status predicted <TM1>
F:343-359/Domain: transmembrane #status predicted <TM2>
F:370-386/Domain: transmembrane #status predicted <TM3>
F:397-413/Domain: transmembrane #status predicted <TM4>
F:442-458/Domain: transmembrane #status predicted <TM5>
F:472-488/Domain: transmembrane #status predicted <TM6>
F:540-556/Domain: transmembrane #status predicted <TM7>
F:873-889/Domain: transmembrane #status predicted <TM8>
F:897-913/Domain: transmembrane #status predicted <TM9>
F:928-944/Domain: transmembrane #status predicted <TM10>
F:972-988/Domain: transmembrane #status predicted <TM11>
F:1009-1025/Domain: transmembrane #status predicted <TM12>

Query Match      15.7%; Score 75; DB 2; Length 1037;
Best Local Similarity 26.2%; Pred. No. 31;
Matches 27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;

QY      7  NFAGIEA-----AASAIQGNVTSIHSL-----DEGKSLTKLAARWGGSGSEAYQGV 53
Db      48  NYPGASQATLNTVTVIEQNMTGLDNLMTSSQSGTGQASVT-LSFKAGTDPDEAVQQ 106

QY      54  VQKWDATATLNNALQNLARTISEAGQ-----AMASTEAGNV 90
Db      107  VQNLQASAMRKLPAQVQNGVTVRKGTDLTLLTAFVSTDGSM 149

Query Match      15.7%; Score 75; DB 2; Length 1037;
Best Local Similarity 26.2%; Pred. No. 31;
Matches 27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;

QY      7  NFAGIEA-----AASAIQGNVTSIHSL-----DEGKSLTKLAARWGGSGSEAYQGV 53
Db      48  NYPGASQATLNTVTVIEQNMTGLDNLMTSSQSGTGQASVT-LSFKAGTDPDEAVQQ 106

QY      54  VQKWDATATLNNALQNLARTISEAGQ-----AMASTEAGNV 90
Db      107  VQNLQASAMRKLPAQVQNGVTVRKGTDLTLLTAFVSTDGSM 149
```

```
RESULT 14
G85889
A:hypothetical protein acrD [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85889
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85889
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1037 <STO>
A:Cross-references: GB:AE005174; NID:g12516848; PIDN:AAAG57579.1; GSPDB:GN00145; UWGP:237
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: acrD
C:Superfamily: acriflavin resistance protein

Query Match      15.7%; Score 75; DB 2; Length 1037;
Best Local Similarity 26.2%; Pred. No. 31;
Matches 27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;

QY      7  NFAGIEA-----AASAIQGNVTSIHSL-----DEGKSLTKLAARWGGSGSEAYQGV 53
Db      48  NYPGASQATLNTVTVIEQNMTGLDNLMTSSQSGTGQASVT-LSFKAGTDPDEAVQQ 106

QY      54  VQKWDATATLNNALQNLARTISEAGQ-----AMASTEAGNV 90
Db      107  VQNLQASAMRKLPAQVQNGVTVRKGTDLTLLTAFVSTDGSM 149

RESULT 15
G96937
A:cell wall-associated hydrolase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: G96937
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: G96937
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78290.1; PID:g15023152; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0309

Query Match      15.3%; Score 73.5; DB 2; Length 371;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 24; Conservative 17; Mismatches 32; Indels 11; Gaps 3;

QY      10  GIEAASAIQGNVTSIHSLDEGKSLTKLAARWGGSGSEAYQGVQKWDATAT---ELN 66
Db      13  GITVSCS---GNIVFASPLQDQYNQSQQQYQNA-----LKSVDIENKIEALDNQIGELN 64

QY      67  NALQNLARTISEAGQAMASTEAGNV 90
Db      65  NSINDTDKRINESQNMAITQGKI 88

RESULT 16
B83566
A:probable bacteriophage protein PA0641 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
```

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83566
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Berman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
A:Reference: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen. Nature 406, 959-964, 2000
A:Accession: B83566
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1204 <STO>
A:Cross-references: GB:AE004499; GB:AE004031; NID:g9946508; PIDN:AAG04030.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0641

Query Match 15.2%; Score 73; DB 2; Length 1204;
Best Local Similarity 23.7%; Pred. No. 59;
Matches 23; Conservative 25; Mismatches 35; Indels 14; Gaps 4;

QY 11 TBAASATQGNVTSIHSLDEKQS-----LTKLAAGWGS--RAYQVQKWDATATE 64
DB 993 LEATADAGRTATVRSQRTAQRLDLSASIGGTAASLOEQRTARANADSALAQ 1052
QY 65 LNNALQART-----TSEAGQAMASTEGVTGMFA 95
DB 1053 RIDTVQ--ARTDTNAAQTTSQATSLDGNVKNYS 1087

RESULT 17
T05959
1.3-beta-glucanase (EC 3.2.1.-) Glu5 - soybean (fragment)
C:Species: Glycine max (soybean)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 29-Sep-1999
C:Accession: T05959
R:Jin, W.; Horner, H.T.; Palmer, R.G.; Shoemaker, R.C.
A:Reference: Submitted to the EMBL Data Library, November 1997
A:Description: Soybean beta-1,3-glucanase.
A:Reference number: Z15471
A:Accession: T05959
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-238 <JIN>
A:Cross-references: EMBL:AF034110; NID:g2921319; PIDN:AA04712.1; PID:g2921320
A:Experimental source: strain Minsoy
C:Genetics:
A:Gene: Glu5
C:Superfamily: beta-1,3-glucanase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 15.1%; Score 72.5; DB 2; Length 238;
Best Local Similarity 30.9%; Pred. No. 9.7;
Matches 30; Conservative 15; Mismatches 35; Indels 17; Gaps 5;

QY 12 EAAAGAIQ--NVTSIHSLDEKQSITKLAAA--WGGSGSEAY--QGVQKWDATATELN-- 66
DB 38 EGVQLAIRSGNTEVILGVNDQLSITNAGATNWNKVKAYSQNVKRYIAGVNEIHP 97
QY 67 -----NALQNLARTISEA---GQAMASTEGNVT 91
DB 98 GDSLAGSVLPALENTQKAISSANLQGMKVSTADITD 134

RESULT 18
A43582
Surface antigen msp1 beta chain - *Anaplasma marginale*
C:Species: *Anaplasma marginale*
C>Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 08-Oct-1999
C:Accession: A43582
R:Barbet, A.F.; Allred, D.R.
A:Reference: Infect. Immun. 59, 971-976, 1991
A:Title: The msp1beta multigene family of *Anaplasma marginale*: nucleotide sequence analysis

A:Reference number: A43582; MUID:911147241; PMID:1671779
A:Accession: A43582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-756 <BAR>
A:Cross-references: GB:M59845; NID:g142172; PIDN:AAA22066.1; PID:g142173
C:Keywords: surface antigen

Query Match 15.1%; Score 72.5; DB 2; Length 756;
Best Local Similarity 21.7%; Pred. No. 38;
Matches 18; Conservative 18; Mismatches 40; Indels 7; Gaps 1;

QY 8 FAGTEAAASATQGNVTSIHSLDEKQSITKLAAAAGSGSEAYQGVQKWDATATELN 67
DB 383 FGSIMTCAKLMKGSFAAINQKFEINATLTREA-----TDIAQGVKETYQSIGDAF 435

QY 68 ALQNLARTISEAGQAMASTEGNV 90
DB 436 AFKSVGDFAFKSIGDAFKSANDGI 458

RESULT 19
DB3771
Hypothetical protein BH0972 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: DB3771
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hino, T.
A:Reference: Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and its relationship to other members of the family Halobacteriaceae.
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: DB3771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <STO>
A:Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA804691.1; GSPDB:GN0
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0972

Query Match 15.0%; Score 72; DB 2; Length 96;
Best Local Similarity 21.4%; Pred. No. 3.7;
Matches 21; Conservative 16; Mismatches 43; Indels 18; Gaps 3;

QY 1 MTEQWNPAGIEAAASATQGNVTSIHSLDEKQSITKLAAAAGSGSEAYQGVQKWD 60
DB 6 MTPPE-----LFTANETRSDAASYQDILLQRGDARIEKLGSTWEG---EAFQGAQWOD 57

QY 61 TATELNALQ-----NLARTISEAGQAMASTEG 88
DB 58 KRKHVEELLQLYEELGAQTDDIANVVTDDQEIRSRIG 95

RESULT 20

C87322

methyl-accepting chemotaxis protein McpG [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: C87322
R:Niermar, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolch, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:211173698; PMID:11259647
A:Accession: C87322
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-637 <STO>
A:Cross-references: GB:AE005673; NID:g13421789; PIDN:AAK22575.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC0589
C:Superfamily: methyl-accepting chemotaxis protein mcpA

Query Match 15.0%; Score 72; DB 2; Length 637;
Best Local Similarity 25.5%; Pred. No. 35;
Matches 24; Conservative 16; Mismatches 42; Indels 12; Gaps 3;

QY 9 AGTEAASAIQGN-----VTSIHLLDEGKQSLTKLAAAGGSGSEAYQGVQKWDATAT 63
DB 476 AGVEAARAGSGRGFAVVAQEVFSLAQRSQAQREITALVNSARADVAAQGGREV-SSTGA 534

QY 64 ELNN-----ALQNLARTISEAGQAMASTEGNVT 91
DB 535 ALNAIVSRVLEIHLVTRISASNEAQAQGTIGSIT 568

RESULT 21
F75605
minor tail protein gp26-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75605
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999.
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: F75605
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1225 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12240.1; PID:g646053
A:Experimental source: strain R1
A:Gene: DRA0108
A:Map position: 2

Query Match 15.0%; Score 72; DB 2; Length 1225;
Best Local Similarity 29.3%; Pred. No. 75;
Matches 27; Conservative 15; Mismatches 36; Indels 14; Gaps 4;

QY 9 AGTEAASAIQGNVTST-----HSLLDEGKQSLTKLAAAGGSGSEAYQGVQKWDAT 61
DB 53 AGTIAAGLLATGAVTAVVGSTVGLQAQAAQVNDFOAKLGASREEA-----EKLGTV 107

QY 62 ATELNALQNLARTISEAGQAMASTEGNVTGM 93
DB 108 AEQVFG--DNWTSLSSEAGEAVANVRVKGL 137

RESULT 22
T00079
hypothetical protein KIAA0465 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00079
R:Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: Z14085; MUID:98116662; PMID:9455484
A:Accession: T00079
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1697 <SEK>
A:Cross-references: EMBL:AB007934; NID:g3413891; PIDN:BAA32310.1; PID:g3413892
A:Experimental source: brain
C:Genetics:
A:Map position: 1
A:Note: KIAA0465

Query Match 15.0%; Score 72; DB 2; Length 1697;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
Matches 24; Conservative 14; Mismatches 28; Indels 22; Gaps 3;

QY 16 SAIQGNVTSIHSLLDGKQSLTKLAAAGGSGSEAYQGV---QOKWDAT----- 61
DB 689 SOLKAKEETYNQLDKGR--LMLLSRDDSGSGSKTEQSVALLQKWHVSSKMEERKSKL 746

QY 62 -----ATELNALQNLARTISEAGQAM 83
DB 747 EEALNLFATEFQNSLQEFINWLTIAEQSL 774

RESULT 23
B89921
hypothetical protein ebha [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89921
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89921
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6713 <KUR>
A:Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: ebha

Query Match 15.0%; Score 72; DB 2; Length 6713;
Best Local Similarity 30.9%; Pred. No. 5.5e+02;
Matches 21; Conservative 15; Mismatches 26; Indels 6; Gaps 2;

QY 14 AASAIQGNVTSIHSLLDGKQSLTKLAAAGGSGSEAYQGVQKWDATATLNALQNL 73
DB 1338 AKTTAKNNLNLTSSINNAQKDALTR-----NIDGATTVAGVNOE-TAKATELNAMHSLO 1391

QY 74 RTISEAGQ 81
DB 1392 NGINDETQ 1399

RESULT 24
D70608
hypothetical protein Rv1198 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: D70608
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70608
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-94 <COL>
A:Cross-references: GB:Z93777; GB:AL123456; NID:g3261726; PIDN:CAB07821.1; PID:e311075;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv1198

Query Match 14.9%; Score 71.5; DB 2; Length 94;
Best Local Similarity 25.5%; Pred. No. 4.1;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLLDGKQSLTK-----LAAA--WGGSGSEAYQGV----- 53
DB 5 YQGDVDVAHGAMIRAQA-----GLLEAEHQAIIRDVLVTASDFWGGAGSACQGFITQLGRN 60

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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:25:57 ; Search time 4.52381 Seconds
(without alignments)
987.561 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQWNPAGIEAAASAIQG.....ISEACQAMASTEGNVTGMFA 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127825

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	474	99.0	94	1	ESA6_MYCTU
2	186	38.8	95	1	ESA6_MYCTU
3	96	20.0	96	1	ESA6_MYCTU
4	81	16.9	96	1	ESA6_MYCTU
5	80.5	16.8	90	1	ESA6_MYCTU
6	80	16.7	95	1	CPFP MYCTU
7	80	16.7	1037	1	FLIC_ECOLI
8	75	15.7	1037	1	ACRD_ECOLI
9	75	15.7	5327	1	MACF_MOUSE
10	72	15.0	5430	1	MACF_HUMAN
11	72	15.0	5938	1	MAC4_HUMAN
12	71.5	14.9	94	1	ESA6_MYCTU
13	71.5	14.9	139	1	CSMC_CHLVE
14	71	14.8	416	1	FTSY_NEIGO
15	70.5	14.7	94	1	ESA6_MYCTU
16	70.5	14.7	94	1	ESA6_MYCTU
17	70.5	14.7	94	1	ESA6_MYCTU
18	70.5	14.7	139	1	CSMC_CHLVI
19	70.5	14.7	388	1	MRP4_STRPY
20	70.5	14.7	2073	1	FAS1_SCHPO
21	70	14.6	103	1	ESA6_MYCTU
22	70	14.6	649	1	VATI_METMA
23	69.5	14.5	382	1	IPAC_SHIDI
24	68	14.2	409	1	GUB_BACCI
25	68	14.2	486	1	CUG1_HUMAN
26	68	14.2	486	1	CUG1_MOUSE
27	68	14.2	706	1	ADGG_HUMAN
28	68	14.2	2564	1	SPCQ_HUMAN
29	67	14.0	550	1	FLIC_SHIFL
30	67	14.0	1063	1	SPTS_YEAST
31	67	14.0	1738	1	CO4_MOUSE
32	67	14.0	2349	1	TPR_HUMAN
33	67	14.0	3718	1	LMA5_MOUSE

34	66.5	13.9	227	1	DJB8_MOUSE
35	66.5	13.9	454	1	XYLX_PSEPU
36	66.5	13.9	457	1	Y162_UREPA
37	66	13.8	185	1	TD52_MOUSE
38	66	13.8	526	1	NABD_MYCLE
39	66	13.8	530	1	YA9A_SCHPO
40	65.5	13.7	137	1	MBB2_ECOLI
41	65.5	13.7	465	1	LIPP_HUMAN
42	65.5	13.7	625	1	DNAK_HALME
43	65.5	13.7	5171	1	BPEA_HUMAN
44	65	13.6	95	1	ES6X_MYCLE
45	65	13.6	307	1	LIPA_CHLEN
46	65	13.6	390	1	FLAA_BORBR
47	65	13.6	430	1	AROA_MYCLE
48	65	13.6	692	1	MYG_PODCA
49	65	13.6	836	1	VG26_BPMO2
50	64.5	13.5	461	1	US45_LACLC
51	64.5	13.5	640	1	DNAK_VIBHA
52	64.5	13.5	890	1	MUTS_RICGN
53	64.5	13.5	918	1	YVJB_CABEL
54	64.5	13.5	1050	1	LKTA_ACTAC
55	64.5	13.5	3695	1	LMA5_HUMAN
56	64	13.4	189	1	CAYP_HUMAN
57	64	13.4	421	1	FTSY_NEIMC
58	64	13.4	712	1	PAL2_TORAC
59	64	13.4	1319	1	BCC1_ACEXY
60	64	13.4	1392	1	CND1_MOUSE
61	63.5	13.3	228	1	DPA5_BPRE9
62	63.5	13.3	328	1	SGS3_DROHR
63	63.5	13.3	483	1	COBQ_VIBPA
64	63.5	13.3	975	1	KINH_DROME
65	63.5	13.3	1816	1	LMA4_MOUSE
66	63	13.2	194	1	HAM1_CAUCR
67	63	13.2	348	1	CTH2_MOUSE
68	63	13.2	348	1	LFXD_NEIMB
69	63	13.2	390	1	CARP_SACFI
70	63	13.2	461	1	SELA_HAEIN
71	63	13.2	504	1	AMPX_VIBPR
72	63	13.2	705	1	STT3_HUMAN
73	63	13.2	705	1	STT3_MOUSE
74	63	13.2	778	1	HTR6_HALN1
75	63	13.2	778	1	HTR6_HALSA
76	63	13.2	6885	1	SNE2_HUMAN
77	62.5	13.0	312	1	CVSK_SYNY3
78	62.5	13.0	395	1	FLA2_RHIME
79	62.5	13.0	395	1	FLB2_RHIME
80	62.5	13.0	527	1	NCF2_BOVIN
81	62.5	13.0	635	1	DNAK_VIBCH
82	62.5	13.0	852	1	VTBR_HSVI1
83	62.5	13.0	879	1	ORP5_HUMAN
84	62.5	13.0	953	1	LKA3_PASHA
85	62	12.9	130	1	RR11_CVAPA
86	62	12.9	185	1	VATE_DEIRA
87	62	12.9	200	1	AKIP_MOUSE
88	62	12.9	242	1	DJB3_MOUSE
89	62	12.9	269	1	PANB_COREP
90	62	12.9	284	1	TPME_CIOIN

ALIGNMENTS

RESULT 1
ESA6_MYCTU STANDARD; PRT; 94 AA.
ID _ESA6_MYCTU
AC Q57165; O84901;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 6 kDa early secretory antigenic target (ESAT-6).
GN ESAT6 OR RV31875 OR MT3989 OR MT027.10.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.

Q9qv17 mus musculus
P23099 pseudomonas
Q9pvy2 ureaplasma
Q62393 mus musculus
Q49617 mycobacteri
P07188 schizosacch
P07113 escherichia
P16233 homo sapien
Q9nhb9 halobacteri
Q94833 homo sapien
Q49946 mycobacteri
Q92774 chlamydia p
Q06064 bordetella
Q06ci3 mycobacteri
Q05000 podocoryne
P22820 mycobacteri
P22865 lactococcus
O87384 vibrio harv
Q92119 rickettsia
P34487 caenorhabdi
P14662 actinobacil
O15230 homo sapien
Q13938 homo sapien
O30391 neisseria m
P35513 nicotiana t
P19450 acetobacter
O84224 mus musculus
O80164 bacterioph
P13730 drosophila
Q87hm1 vibrio para
P17210 drosophila
P97927 mus musculus
Q9abs4 caulobacter
Q9cyc5 mus musculus
P95377 neisseria m
P22929 saccharomyc
P43910 haemophilus
Q01693 vibrio prot
P46977 homo sapien
P46978 mus musculus
Q9hr92 halobacteri
Q48319 halobacteri
Q8wxh0 homo sapien
P73410 synecocyst
P13118 rhizobium m
P13119 rhizobium m
O7775 bos taurus
Q34241 vibrio chol
Q00140 ictaluriid h
Q9h0x9 homo sapien
P55116 pasteurella
P48136 cyanophora
Q9rwh1 deinococcus
Q9dcj7 mus musculus
Q35723 mus musculus
Q8fua5 corynebacte
Q7068 ciona intes

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773, 1765;
 RN [1]
 RC SPECIES=FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;
 RX MEDLINE=95204931; PubMed=7897219;
 RA Andersen P., Andersen A.B., Sorensen A.L., Nagai S.;
 RA "Recall of long-lived immunity to Mycobacterium tuberculosis infection
 in mice.";
 RL J. Immunol. 154:3359-3372(1995).
 RN [2]
 RN SEQUENCE FROM N.A., SEQUENCE OF 1-10, AND CHARACTERIZATION.
 RC SPECIES=M.tuberculosis; STRAIN=Ersmann;
 RX MEDLINE=95247251; PubMed=7729876;
 RA Sorensen A.L., Nagai S., Hoven G., Anderson P., Anderson A.B.;
 RA "Purification and characterization of a low-molecular-mass T-cell
 antigen secreted by Mycobacterium tuberculosis.";
 RT Infect. Immun. 63:1710-1717(1995).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.B., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RT Nature 393:537-544(1998).
 RL [4]
 RN [5]
 RN SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RC SPECIES=M.tuberculosis;
 RA Singh B., Siddiqui Z., Singh S., Sharma P.;
 RA "ESAT-6 gene of a clinical isolate of Mycobacterium tuberculosis from
 India.";
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=M.bovis;
 RX MEDLINE=96200095; PubMed=8631702;
 RA Mahairas G.G., Sabo P.J., Hickey M.J., Singh D.C., Stover C.K.;
 RA "Molecular analysis of genetic differences between Mycobacterium bovis
 BCG and virulent M. bovis.";
 RL J. Bacteriol. 178:1274-1282(1996).
 RN [7]
 RN SEQUENCE OF 1-70 FROM N.A.
 RC SPECIES=M.tuberculosis; STRAIN=H37RV;
 RX MEDLINE=99061212; PubMed=9846755;
 RA Berthet F.-X., Rasmussen P.B., Rosenkrands I., Andersen P.,
 RA Gicquel B.;
 RA "A Mycobacterium tuberculosis operon encoding ESAT-6 and a novel
 low-molecular-mass culture filtrate protein (CFP-10).";
 RL Microbiology 144:3195-3203(1998).
 CC CC -1- FUNCTION: NOT KNOWN. ELICITS HIGH LEVEL OF INF-GAMMA FROM MEMORY
 CC EFFECTOR CELLS DURING THE FIRST PHASE OF A PROTECTIVE IMMUNE
 CC RESPONSE.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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 CC -----
 DR EMBL; U34848; AAC44033.1; -;
 DR EMBL; X79562; CAA56099.1; -;
 DR EMBL; AL022120; CAAL7967.1; -;
 DR EMBL; AF420491; AAL16896.1; -;
 DR EMBL; AE007190; AAK48357.1; -;
 DR EMBL; AF004671; AAC83446.1; -;
 DR PIR; A70803; A70803.
 DR TIGR; MT3989; -;
 DR Tuberculist; Rv3875; -;
 KW Antigen; Complete proteome.
 FT INIT MET 0
 SQ SEQUENCE 94 AA; 9773 MW; 19245B05C478BC84 CRC64;
 Query Match 99.0%; Score 474; DB 1; Length 94;
 Best Local Similarity 100.0%; Pred. No. 9e-41;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKWDAT 61
 DB 1 TEQOWNFAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAWGGSGSEAYQGVQKWDAT 60
 QY 62 ATELNNALQNLAITISEAGQAMASTEIGNVTGMFA 95
 DB 61 ATELNNALQNLAITISEAGQAMASTEIGNVTGMFA 94
 RESULT 2
 ESA6 MYCLE
 ID ESA6 MYCLE STANDARD; PRT; 95 AA.
 AC Q50206; Q503083;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 6 kDa early secretory antigenic target homolog (ESAT-6-like protein)
 DE (L-ESAT)
 GN ESA6 OR ESX OR L45 OR ML0049 OR MLCB628.12C.
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP Wielebs B., Notenboom T., Naafs B., Offringa R., Ottenhoff T.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eigemeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RA "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
 CC -----
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DR EMBL; AL021930; CAA17363.1; -
DR EMBL; AE006937; AAK44525.1; -
DR PIR; F70836; F70836.
DR TIGR; MT0301; -.
DR Tuberculin; RV0288; -.
KW Antigen; Complete proteome.
FT INIT MET 0
SQ SEQUENCE 95 AA; 10259 MW; 25D727778090F47E CRC64;

Query Match 16.7%; Score 80; DB 1; Length 95;
Best Local Similarity 29.7%; Pred. No. 0.2;
Matches 27; Conservative 12; Mismatches 40; Indels 12; Gaps 3;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAGGSGSEAYQGVQKWDATATL 65
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
5 YNPAMLGHAGDMYAGTGLQSLGAEIAVEQALQASMGQDGTGITYQAWQAW----- 57
QY 66 NNALQNLARTTISEAGQAMAST-EGNVVTGMFA 95
Db ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
58 NQAMEDLYR-----AYHMSSTHEANTMAMA 84

RESULT 7
FLIC_ECOLI
ID FLIC_ECOLI STANDARD; PRT; 497 AA.
AC P04949;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Flagellin.
GN FLIC OR FLAF OR HAG OR B1923.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI TaxID=562;
FN SEQUENCE FROM N.A.
RP STRAIN=K12;
RX MEDLINE=87057066; PubMed=3536885;
RA Kuwajima G., Asaka J.-I., Fujiwara T., Fujiwara T., Node K., Kondo E.;
RT "Nucleotide sequence of the hag gene encoding flagellin of
RT Escherichia coli.";
RL J. Bacteriol. 168:1479-1483(1986).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=89281489; PubMed=2659972;
RA Hanafusa T., Sakai A., Tominaga A., Enomoto M.;
RT "Isolation and characterization of Escherichia coli hag operator
RT mutants whose hag48 expression has become repressible by a Salmonella
RT H1 repressor.";
RL Mol. Gen. Genet. 216:44-50(1989).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RL "A 460-kb DNA sequence of the Escherichia coli K-12 genome
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RL "A 460-kb DNA sequence of the Escherichia coli K-12 genome
[5]
corresponding to the 40.1-50.0 min region on the linkage map.";
DNA Res. 3:379-392(1996).
[6]
SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=83238225; PubMed=6305924;
RA Szekely E., Simon M.;
RT "DNA sequence adjacent to flagellar genes and evolution of flagellar-
RT phase variation.";
RL J. Bacteriol. 155:74-81(1983).
[7]
SEQUENCE OF 1-12.
RP STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
[8]
SEQUENCE OF 1-4.
RP STRAIN=K12 / W3110;
RX MEDLINE=98263247; PubMed=9600841;
RA Wilkins M.R., Gasteiger E., Tonella L., Ou K., Tyler M.,
RA Sanchez J.-C., Gooley A.A., Walsh B.J., Bairoch A., Appel R.D.,
RA Williams K.L., Hochstrasser D.F.;
RT "Protein identification with N and C-terminal sequence tags in
RT proteome projects.";
RL J. Mol. Biol. 278:599-608(1998).
[9]
FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
[10]
SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
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[11]
EMBL; M14358; AAA23950.1; -
EMBL; X17440; CAA35488.1; -
EMBL; AE000285; AAC74990.1; -
EMBL; D90832; BAA15744.1; -
EMBL; D90833; BAA15751.1; -
EMBL; J01607; BAA92491.1; -
PIR; A37249; FLEC.
SWISS-2DPAGE; P04949; COLI.
Ecogen; EG10321; flic.
InterPro; IPR001029; Flagellin C.
InterPro; IPR001492; Flagellin N.
Pfam; PF00700; Flagellin_C_1.
Pfam; PF00669; Flagellin_N_1.
PRINTS; PR00207; FLAGELLIN.
Flagella; Complete proteome.
FT INIT MET 0
FT CONFLICT 284 284 P -> L (IN REF. 2).
SQ SEQUENCE 497 AA; 51163 MW; 24B5419C21C7B4E8 CRC64;

Query Match 16.7%; Score 80; DB 1; Length 497;
Best Local Similarity 30.4%; Pred. No. 1.4;
Matches 24; Conservative 9; Mismatches 38; Indels 8; Gaps 1;

QY 9 AGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAGGSGSEAYQGVQKWDATATL 68
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
393 AGGALTVANGKTDPDKALDDAIAVDFKRSILG-----AVQNRILDSAVTNLNT 444
QY 69 LQNLARTTISEAGQAMASTE 87
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
445 TTNLSEAQSRIDQADYATE 463

RESULT 8
ACRD_ECOLI

```

ACRD ECOLI STANDARD; PRT: 1037 AA.
 P24177; P76971; P77178; Q46715;
 01-MAR-1992 (Rel. 21, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable aminoglycoside efflux pump (Acriflavine resistance protein
 D).
 GN ACRD OR B2470.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Nilles M.L., Bertrand K.P.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RA Ma D., Cook D.N., Alberti M., Nikaido H., Hearst J.E.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Mau B., Shao Y.;
 RL "The complete genome sequence of Escherichia coli K-12.";
 Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=97349980; PubMed=9205837;
 RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
 Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsushashi N.,
 Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
 Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 Yamagata S., Horiuchi T.;
 RA "Construction of a contiguous 874-Kb sequence of the Escherichia coli
 K-12 genome corresponding to 50.0-68.8 min on the linkage map and
 analysis of its sequence features.";
 DNA Res. 4:91-113(1997).
 RN [5]
 RP SEQUENCE OF 998-1037 FROM N.A.
 RC STRAIN=K12;
 RA MEDLINE=92355499; PubMed=1644752;
 RA Bouvier J., Richard C., Higgins W., Bogler O., Stragier S.;
 RL "Cloning, characterization, and expression of the dapE gene of
 Escherichia coli.";
 J. Bacteriol. 174:5265-5271(1992).
 RN [6]
 RP FUNCTION.
 RA MEDLINE=20158894; PubMed=10692383;
 RA Rosenberg E.Y., Ma D., Nikaido H.;
 RL "Acrd of Escherichia coli is an aminoglycoside efflux pump.";
 J. Bacteriol. 182:1754-1756(2000).
 CC -!- FUNCTION: PARTICIPATES IN THE EFFLUX OF AMINOGLYCOSIDES. CONFERS
 CC RESISTANCE TO A VARIETY OF THESE SUBSTANCES.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (BY similarity).
 CC -!- SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.
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DR EMBL; U12598; AAA20584.1; -;
 DR EMBL; U10436; AAA74741.1; -;
 DR EMBL; AE000334; AAC75523.1; -;
 DR EMBL; D90875; BAA16344.1; -;
 DR EMBL; D90876; BAA16348.1; -;
 DR EMBL; X57403; BAA40663.1; -;
 DR PIR; B65022; B65022.
 DR EcoGene; EG10014; acrd.
 DR InterPro; IPR001036; Acrflvin_res.
 DR InterPro; IPR004764; HAE1.
 DR Pfam; PF00873; ACR_tran; 1.
 DR PRINTS; PRO0702; ACRIFLAVINRP.
 DR TIGRFAMs; TIGR00915; 2A0602; 1.
 KW Transmembrane; Inner membrane; Transport; Complete proteome.
 FT DOMAIN 1 9
 FT TRANSMEM 10 28
 FT DOMAIN 29 339
 FT TRANSMEM 340 359
 FT DOMAIN 360 365
 FT TRANSMEM 366 385
 FT DOMAIN 386 391
 FT TRANSMEM 392 413
 FT DOMAIN 414 441
 FT TRANSMEM 442 460
 FT DOMAIN 461 473
 FT TRANSMEM 474 496
 FT DOMAIN 497 537
 FT TRANSMEM 538 556
 FT DOMAIN 557 870
 FT TRANSMEM 871 890
 FT DOMAIN 891 896
 FT TRANSMEM 897 916
 FT DOMAIN 917 922
 FT TRANSMEM 923 944
 FT DOMAIN 945 971
 FT TRANSMEM 972 990
 FT DOMAIN 991 1003
 FT TRANSMEM 1004 1026
 FT DOMAIN 1027 1037
 FT CONFLICT 303 303
 FT CONFLICT 372 372
 FT CONFLICT 385 385
 FT CONFLICT 461 461
 FT CONFLICT 665 665
 FT CONFLICT 763 763
 FT CONFLICT 775 775
 FT CONFLICT 778 778
 SQ SEQUENCE 1037 AA; 113047 MW; 961611E1D24FD4E5 CRC64;
 Query Match 15.7%; Score 75; DB 1; Length 1037;
 Best Local Similarity 26.2%; Pred. No. 10;
 Matches 27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;
 QY 7 NFAGIEA-----AASAIQGNVTSHLL-----DEGQSILKLAAGWGSSEAYQG 53
 Db 48 NYPGASQTLNVTQVIEQNTGLDNLNMYMSQSSGTQASVT-LSFKAGTDPDEAVQQ 106
 QY 54 VQCKWDATATLNALONLARTISEAQ-----AMASTEGRV 90
 Db 107 VQNKQAMRKUPQAVQNGVTVRKGTGDTNLTIAFVSDGSM 149
 RESULT 9
 MACF_MOUSE STANDARD; PRT: 5327 AA.
 ID MACF_MOUSE
 AC Q9QXZ0; P97394; P97395; P97396;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Microtubule-actin crosslinking factor 1 (Actin cross-linking family
 DE 7).
 GN MACF1 OR MACF OR ACF7 OR ACFP7.
 OS Mus musculus (Mouse).

DR SMART; SM00150; SPEC; 36.
 DR PROSITE; PS00019; ACTININ_1; 1.
 DR PROSITE; PS00020; ACTININ_2; FALSE_NEG.
 DR PROSITE; PS00021; CH; 2.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00002; SH3; FALSE_NEG.
 KW Actin-binding; Cytoskeleton; Calcium; Calcium-binding; Repeat;
 KW SH3 domain; Coiled coil; Alternative splicing.
 FT DOMAIN 1 295 ACTIN-BINDING.
 FT DOMAIN 78 181 CH 1.
 FT DOMAIN 194 295 CH 2.
 FT DOMAIN 243 265 COILED COIL (POTENTIAL).
 FT DOMAIN 477 529 COILED COIL (POTENTIAL).
 FT DOMAIN 722 751 COILED COIL (POTENTIAL).
 FT DOMAIN 816 843 COILED COIL (POTENTIAL).
 FT DOMAIN 1013 1118 COILED COIL (POTENTIAL).
 FT DOMAIN 1164 1191 COILED COIL (POTENTIAL).
 FT DOMAIN 1399 1690 COILED COIL (POTENTIAL).
 FT DOMAIN 1780 1843 COILED COIL (POTENTIAL).
 FT DOMAIN 1975 2005 COILED COIL (POTENTIAL).
 FT DOMAIN 2039 2312 COILED COIL (POTENTIAL).
 FT DOMAIN 2385 2417 COILED COIL (POTENTIAL).
 FT DOMAIN 2544 2695 COILED COIL (POTENTIAL).
 FT DOMAIN 2760 2838 COILED COIL (POTENTIAL).
 FT DOMAIN 2911 3001 COILED COIL (POTENTIAL).
 FT DOMAIN 3130 3164 COILED COIL (POTENTIAL).
 FT DOMAIN 3244 3277 COILED COIL (POTENTIAL).
 FT DOMAIN 3418 3482 COILED COIL (POTENTIAL).
 FT DOMAIN 3596 3666 COILED COIL (POTENTIAL).
 FT DOMAIN 3786 3806 COILED COIL (POTENTIAL).
 FT DOMAIN 3852 3931 COILED COIL (POTENTIAL).
 FT DOMAIN 3967 3987 COILED COIL (POTENTIAL).
 FT DOMAIN 4084 4218 COILED COIL (POTENTIAL).
 FT DOMAIN 4343 4378 COILED COIL (POTENTIAL).
 FT DOMAIN 4408 4437 COILED COIL (POTENTIAL).
 FT DOMAIN 4468 4498 COILED COIL (POTENTIAL).
 FT DOMAIN 4907 4935 COILED COIL (POTENTIAL).
 FT DOMAIN 5044 5067 COILED COIL (POTENTIAL).
 FT REPEAT 314 355 SPECTRIN 1.
 FT REPEAT 591 623 SPECTRIN 2.
 FT REPEAT 680 784 SPECTRIN 3.
 FT REPEAT 786 800 SPECTRIN 4.
 FT DOMAIN 871 923 SH3.
 FT REPEAT 1250 1272 SPECTRIN 5.
 FT REPEAT 1287 1342 SPECTRIN 6.
 FT REPEAT 1455 1534 SPECTRIN 7.
 FT REPEAT 1547 1659 SPECTRIN 8.
 FT REPEAT 1815 1891 SPECTRIN 9.
 FT REPEAT 1932 2042 SPECTRIN 10.
 FT REPEAT 2260 2280 SPECTRIN 11.
 FT REPEAT 2372 2395 SPECTRIN 12.
 FT REPEAT 2398 2507 SPECTRIN 13.
 FT REPEAT 2510 2618 SPECTRIN 14.
 FT REPEAT 2621 2728 SPECTRIN 15.
 FT REPEAT 2731 2838 SPECTRIN 16.
 FT REPEAT 2841 2945 SPECTRIN 17.
 FT REPEAT 2987 3024 SPECTRIN 18.
 FT REPEAT 3136 3163 SPECTRIN 19.
 FT REPEAT 3187 3274 SPECTRIN 20.
 FT REPEAT 3277 3383 SPECTRIN 21.
 FT REPEAT 3386 3492 SPECTRIN 22.
 FT REPEAT 3495 3601 SPECTRIN 23.
 FT REPEAT 3604 3673 SPECTRIN 24.
 FT REPEAT 3713 3819 SPECTRIN 25.
 FT REPEAT 3832 3927 SPECTRIN 26.
 FT REPEAT 3982 4043 SPECTRIN 27.
 FT REPEAT 4046 4152 SPECTRIN 28.
 FT REPEAT 4155 4262 SPECTRIN 29.
 Query Match
 Best Local Similarity 27.3%; Pred. No. 1.4e+02;
 Matches 24; Conservative 14; Mismatches 28; Indels 22; Gaps 3;

QY 16 SAIQCNVTSIHLLDEGKQSLTKLAAWGGSGSEAYQGV---QQKWDAT----- 61
 DB 4422 SQLKAKEETYNQLLDKGR-LWLLSRDDSGSGKSTEQSVALLQKHVVSSKWERKSKL 4479
 QY 62 -----ATELNALNQLARTISEAQAM 83
 DB 4480 BEALNLATEFQNSLQEFINWLTLAQSL 4507
 RESULT 11
 MAC4_HUMAN
 ID MAC4_HUMAN STANDARD; PRT; 5938 AA.
 AC Q96PK2; Q8WXY1;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Microtubule-actin crosslinking factor 1, isoform 4.
 GN MACF1 OR ACF7 OR ABP620 OR KIAA0465 OR KIAA1251.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RX MEDLINE=21833812; PubMed=11845288;
 RA Gong T.-W.L., Besirli C.G., Lomax M.I.;
 RT Mamm. Genome 12:852-861(2001).
 CC -!- FUNCTION: May play a role in cross-linking cytoskeletal proteins
 by binding intermediate filaments to the N-terminal plectin
 repeats and microtubules to the C-terminus.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=4;
 CC IsoId=Q96PK2-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=Q9UPN3-1; Sequence=External;
 CC Name=2;
 CC IsoId=Q9UPN3-2; Sequence=External;
 CC Name=3;
 CC IsoId=Q9UPN3-3; Sequence=External;
 CC -!- TISSUE SPECIFICITY: Expressed in heart, lung, pituitary and
 placenta, not found in brain, kidney, liver, pancreas or skeletal
 muscle.
 CC -!- SIMILARITY: Belongs to the plakin or cytolinker family.
 CC -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC -!- SIMILARITY: Contains 19 plectin repeats.
 CC -!- SIMILARITY: Contains 32 spectrin repeats.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF317696; AAL09459.1; -
 DR EMBL; AF325341; AAL38997.1; -
 DR EMBL; AF325333; AAL38997.1; JOINED.
 DR EMBL; AF325334; AAL38997.1; JOINED.
 DR EMBL; AF325335; AAL38997.1; JOINED.
 DR EMBL; AF325336; AAL38997.1; JOINED.
 DR EMBL; AF325339; AAL38997.1; JOINED.
 DR EMBL; AF325340; AAL38997.1; JOINED.
 DR GO; GO:0008017; F: microtubule binding; ISS.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR003108; GAS2.
 DR InterPro; IPR001101; Plectin_repeat.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00036; ehand; 2.
 DR Pfam; PF02187; GAS2; 1.

DR Pfam; PF00681; Plectin; 11.
DR Pfam; PF00435; spectrin; 26.
DR ProDom; PD000012; EF-hand; 1.
DR SMART; SM00054; EFh; 2.
DR SMART; SM00243; GAS2; 1.
DR SMART; SM00250; PLEC; 19.
DR SMART; SM00150; SPEG; 32.
DR PROSITE; PS00018; EF_HAND; 2.
KW Cytoskeleton; Calcium; Calcium-binding; Repeat; Coiled coil;
KW Alternative splicing.
FT DOMAIN 1830 1936 COILED COIL (POTENTIAL).
FT DOMAIN 2001 2192 COILED COIL (POTENTIAL).
FT DOMAIN 2282 2345 COILED COIL (POTENTIAL).
FT DOMAIN 2477 2507 COILED COIL (POTENTIAL).
FT DOMAIN 2541 2654 COILED COIL (POTENTIAL).
FT DOMAIN 2686 2814 COILED COIL (POTENTIAL).
FT DOMAIN 2887 2919 COILED COIL (POTENTIAL).
FT DOMAIN 3046 3197 COILED COIL (POTENTIAL).
FT DOMAIN 3262 3503 COILED COIL (POTENTIAL).
FT DOMAIN 3632 3666 COILED COIL (POTENTIAL).
FT DOMAIN 3746 3779 COILED COIL (POTENTIAL).
FT DOMAIN 3920 3984 COILED COIL (POTENTIAL).
FT DOMAIN 4098 4168 COILED COIL (POTENTIAL).
FT DOMAIN 4288 4308 COILED COIL (POTENTIAL).
FT DOMAIN 4354 4386 COILED COIL (POTENTIAL).
FT DOMAIN 4397 4433 COILED COIL (POTENTIAL).
FT DOMAIN 4469 4489 COILED COIL (POTENTIAL).
FT DOMAIN 4586 4720 COILED COIL (POTENTIAL).
FT DOMAIN 4845 4880 COILED COIL (POTENTIAL).
FT DOMAIN 4910 4939 COILED COIL (POTENTIAL).
FT DOMAIN 4970 5000 COILED COIL (POTENTIAL).
FT DOMAIN 5409 5437 COILED COIL (POTENTIAL).
FT DOMAIN 5546 5569 COILED COIL (POTENTIAL).
FT CA BIND 5598 5610 EF-HAND 1 (POTENTIAL).
FT CA BIND 5634 5646 EF-HAND 2 (POTENTIAL).
FT REPEAT 12 49 PLECTIN 1.
FT REPEAT 53 88 PLECTIN 2.
FT REPEAT 89 126 PLECTIN 3.
FT REPEAT 130 164 PLECTIN 4.
FT REPEAT 166 202 PLECTIN 5.
FT REPEAT 203 240 PLECTIN 6.
FT REPEAT 243 278 PLECTIN 7.
FT REPEAT 279 316 PLECTIN 8.
FT REPEAT 318 354 PLECTIN 9.
FT REPEAT 375 762 PLECTIN 10.
FT REPEAT 763 800 PLECTIN 11.
FT REPEAT 801 838 PLECTIN 12.
FT REPEAT 839 876 PLECTIN 13.
FT REPEAT 897 934 PLECTIN 14.
FT REPEAT 935 972 PLECTIN 15.
FT REPEAT 975 1011 PLECTIN 16.
FT REPEAT 1012 1049 PLECTIN 17.
FT REPEAT 1121 1158 PLECTIN 18.
FT REPEAT 1159 1196 PLECTIN 19.
FT REPEAT 1925 2032 SPECTRIN 1.
FT REPEAT 2052 2160 SPECTRIN 2.
FT REPEAT 2211 2313 SPECTRIN 3.
FT REPEAT 2320 2430 SPECTRIN 4.
FT REPEAT 2437 2543 SPECTRIN 5.
FT REPEAT 2550 2652 SPECTRIN 6.
FT REPEAT 2659 2758 SPECTRIN 7.
FT REPEAT 2765 2896 SPECTRIN 8.
FT REPEAT 2903 3008 SPECTRIN 9.
FT REPEAT 3015 3119 SPECTRIN 10.
FT REPEAT 3126 3229 SPECTRIN 11.
FT REPEAT 3236 3339 SPECTRIN 12.
FT REPEAT 3346 3445 SPECTRIN 13.
FT REPEAT 3453 3555 SPECTRIN 14.
FT REPEAT 3562 3664 SPECTRIN 15.
FT REPEAT 3671 3775 SPECTRIN 16.
FT REPEAT 3782 3884 SPECTRIN 17.
FT REPEAT 3891 3993 SPECTRIN 18.
FT REPEAT 4000 4102 SPECTRIN 19.

FT REPEAT 4109 4211 SPECTRIN 20.
FT REPEAT 4218 4320 SPECTRIN 21.
FT REPEAT 4327 4428 SPECTRIN 22.
FT REPEAT 4438 4544 SPECTRIN 23.
FT REPEAT 4551 4653 SPECTRIN 24.
FT REPEAT 4660 4763 SPECTRIN 25.
FT REPEAT 4770 4872 SPECTRIN 26.
FT REPEAT 4879 4982 SPECTRIN 27.
FT REPEAT 4989 5091 SPECTRIN 28.
FT REPEAT 5098 5201 SPECTRIN 29.
FT REPEAT 5208 5309 SPECTRIN 30.
FT REPEAT 5316 5418 SPECTRIN 31.
FT REPEAT 5425 5555 SPECTRIN 32.
FT CONFLICT 1712 1712 P -> S (IN REF. 1; AAL38997).
SQ SEQUENCE 5938 AA; 670134 MW; B87841112752DA004 CRC64;

Query Match 15.0%; Score 72; DB 1; Length 5938;
Best Local Similarity 27.3%; Pred. No. 1.5e+02;
Matches 24; Conservative 14; Mismatches 28; Indels 22; Gaps 3;
QY 16 SAIQGVNTSIHSLDEGKSLTKLAAGGSGSEAYQGV---QQKWDAT----- 61
Db 4924 SOLKAEETYNQLLDKGR--LMLSRDSDSGSKTEQSVALLQKHWVSSKMERKSKL 4981
QY 62 -----ATELNALQNLTARTISEAGQAM 83
Db 4982 EEALNLTAEFQNSLQEFINLTLEAQSL 5009

RESULT 12
ES64_MVCTU
ID ES64_MVCTU STANDARD; PRT; 94 AA.
AC 005300;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ESAT-6 like protein 4.
GN RV1198 OR MT1236 OR MTC1364.10.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Horsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
CC
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DR EMBL; Z93777; CAB07821.1; --
DR EMBL; AE007000; AAK45493.1; --
DR PIR; D70608; D70608.
DR TIGR; MT1236; --
DR TubercuList; Rv1198; --
KW Hypothetical protein; Complete proteome.
FT CONFLICT 32 32 I -> V (IN REF. 2).
FT CONFLICT 37 39 TAS -> AAG (IN REF. 2).
SQ SEQUENCE 94 AA; 9928 MW; 5585B30B9488C46C CRC64;

Query Match 14.9%; Score 71.5; DB 1; Length 94;
Best Local Similarity 25.5%; Pred. No. 1.4;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKSLTK--LAAA--WGSGSEAYQG----- 53
D 5 YQGDVDAHGAMIRAQA-----GLAEHQAIIRDVLTASDFWGGAGSAACQGFITQLGRN 60

QY 54 ---VQKWDATATLNNALQNLARTISBAGQAMA 84
D 61 FQVIYEQANAHGQKVOAAGNNAQTDSSAVGSSWA 94

RESULT 13

CSMC CHLITE
ID CSMC_CHLITE STANDARD; PRT; 139 AA.
AC Q46367;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chlorosome protein C (14 kDa chlorosome protein).
GN CSMC OR CT1943.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;

SEQUENCE FROM N.A.
RA Chung S., Frank G., Zuber H., Bryant D.A.;
RT "Genes encoding two chlorosome components from the green sulfur
RT bacteria Chlorobium vibrioforme strain 8327D and Chlorobium
RT tepidum.";
RL Photosyn. Res. 41:261-275 (1994).

FUNCTION AND MUTAGENESIS OF GLY-307.
MEDLINE=99121009; PubMed=9922234;
RA Arvidson C.G., Powers T., Walter P., So M.;
RT "Neisseria gonorrhoeae Pila is an FtsY homolog.";
RL J. Bacteriol. 181:731-739 (1999).
CC -1- FUNCTION: Functional homolog of SRP receptor. Probably involved in
CC the reception and insertion of a subset of proteins at the
CC cytoplasmic membrane (By similarity). Can replace ftsY in a in
CC vitro translocation assay using purified E.coli SRP components.
CC GTPase activity is necessary for its function.
CC -1- COFACTOR: Requires magnesium.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC pili promoter DNA in a sequence-specific manner using gel
CC retardation assay but it cannot be explained.
CC -1- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
CC -1- CAUTION: THIS IS CONCEPTUAL TRANSLATION THAT INTRODUCES A
CC FRAMESHIFT AT POSITION 295 TO RESTORE THE SIMILARITY WITH OTHER
CC PROTEINS OF THIS FAMILY.
CC -1- CAUTION: Was originally (Ref.1) thought to activate the pilin
CC promoter.

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DR EMBL; U09866; AAA18791.1; --

DR EMBL; AE012944; AAM73162.1; --
DR TIGR; CT1943; --
KW Photosynthesis; Bacteriochlorophyll; Chlorosome; Complete proteome.
SQ SEQUENCE 139 AA; 14325 MW; 48A5025C0574824C CRC64;

Query Match 14.9%; Score 71.5; DB 1; Length 139;
Best Local Similarity 20.0%; Pred. No. 2.2;
Matches 21; Conservative 19; Mismatches 52; Indels 13; Gaps 2;

QY 1 MTEQOMNFAGIEAASAIQGNVTSIHSLDEGKSLTKLAAWGGSGSEAYQGVQ----- 55
D 30 LTGQSAIVGGLVAGRVVTVGTGVGSLID--ASGITNIILOGSGGVGGETIDRVAITVKD 87
QY 56 -----QKWDATATLNNALQNLARTISBAGQAMA--TEGNTGMF 94
D 88 VRSAGELYNDVAVRNVENATSNAAKAVGCVGSASEAVKNITAGSF 132

RESULT 14

FTSY NEIGO
ID FTSY NEIGO STANDARD; PRT; 416 AA.
AC P14929;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell division protein ftsY homolog.
GN FTSY OR PILA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11A;
RX MEDLINE=89210824; PubMed=2854063;
RA Taha M.K., So M., Seifert H.S., Billyard E., Marchal C.;
RT "Pilin expression in Neisseria gonorrhoeae is under both positive and
RT negative transcriptional control.";
RL EMO J. 7:4367-4378 (1988).
RN [2]
RP GTPASE ACTIVITY.
RX MEDLINE=96064663; PubMed=7592800;
RA Arvidson C.G., So M.;
RT "The Neisseria transcriptional regulator Pila has a GTPase activity.";
RL J. Biol. Chem. 270:26045-26048 (1995).
RN [3]

FUNCTION AND MUTAGENESIS OF GLY-307.
MEDLINE=99121009; PubMed=9922234;
RA Arvidson C.G., Powers T., Walter P., So M.;
RT "Neisseria gonorrhoeae Pila is an FtsY homolog.";
RL J. Bacteriol. 181:731-739 (1999).
CC -1- FUNCTION: Functional homolog of SRP receptor. Probably involved in
CC the reception and insertion of a subset of proteins at the
CC cytoplasmic membrane (By similarity). Can replace ftsY in a in
CC vitro translocation assay using purified E.coli SRP components.
CC GTPase activity is necessary for its function.
CC -1- COFACTOR: Requires magnesium.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC pili promoter DNA in a sequence-specific manner using gel
CC retardation assay but it cannot be explained.
CC -1- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
CC -1- CAUTION: THIS IS CONCEPTUAL TRANSLATION THAT INTRODUCES A
CC FRAMESHIFT AT POSITION 295 TO RESTORE THE SIMILARITY WITH OTHER
CC PROTEINS OF THIS FAMILY.
CC -1- CAUTION: Was originally (Ref.1) thought to activate the pilin
CC promoter.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X13965; CRA32144.1; ALT_FRAME.
CC HSP; P10121; 1FTS.
CC InterPro; IPR003593; AAA ATPase.
CC InterPro; IPR004390; ABC_transpt_FtsY.
CC InterPro; IPR000897; SRP54.
CC Pfam; PF00448; SRP54; 1.
CC Pfam; PF02881; SRP54 N; 1.
CC ProDom; PD000819; SRP54; 1.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMs; TIGR00064; ftsY; 1.
CC PROSITE; PS00300; SRP54; 1.
CC Signal recognition particle; GRP-binding; RNA-binding; Membrane;
KW Cell division.
FT NP_BIND 224 231 GTP (BY SIMILARITY).
FT NP_BIND 304 308 GTP (BY SIMILARITY).
FT NP_BIND 368 371 GTP (BY SIMILARITY).
FT MUTAGEN 307 307 G->A: DECREASE IN GTPASE ACTIVITY; UNABLE
FT TO COMPLEMENT THE LACK OF FTSY IN E.COLI;
FT NO TRANSLOCATION ACTIVITY.
SQ SEQUENCE 416 AA; 44359 MW; ABD977BAFF79E4ED CRC64;

Query Match 14.8%; Score 71; DB 1; Length 416;
Best Local Similarity 22.6%; Pred.No. 8.8;
Matches 19; Conservative 15; Mismatches 50; Indels 0; Gaps 0;

QY 9 AGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQVQKWDATATLNNNA 68
DB 19 AQVQETAKVESEVAQIVGNIKEDVESLAEKSVKRAESAVETVSGAVEQVKETVAEMPSE 78
QY 69 LQNARTISEAQMASTEGNTG 92
DB 79 AGEAAERVESAKEVAETVGEAVG 102

RESULT 15
ES61_MYCTU STANDARD; PRT; 94 AA.
AC P96364; O08120; O08122; Q9L781;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antigen Mtb9.9B (ESAT-6 like protein 1).
GN (RV1037C OR MT1066 OR MTCY10G2.12) AND
GN (RV3619C OR MT3721 OR MTCY15C10.33 OR MTCY07H7B.03).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Alderson M.R., Bement T., Day C.H., Zhu L., Molesh D., Skeiky Y.A.W.,
RA Coler R., Lewinson D.M., Reed S.G., Dillon D.C.;
RA "Expression cloning of an immunodominant family of Mycobacterium
RA tuberculosis antigens using human CD4(+) T cells.";
RA J. Exp. Med. 191:551-560(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
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RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., S.L.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF226277; AAF32406.1; -.
CC EMBL; Z92539; CAB06842.1; -.
CC EMBL; Z95436; CAB08822.1; -.
CC EMBL; AE006989; AAK45317.1; -.
CC EMBL; AE007171; AAK48082.1; -.
CC PIR; D70560; D70560.
CC TIGR; MT1066; -.
CC TIGR; MT3721; -.
CC Tuberculist; RV1037C; -.
CC Tuberculist; RV3619C; -.
CC Hypothetical protein; Complete proteome.
FT CONFLICT 20 20 Q -> L (IN REF. 1 AND 3; AAK48082).
FT CONFLICT 23 23 S -> L (IN REF. 1 AND 3; AAK48082).
SQ SEQUENCE 94 AA; 9833 MW; 8F971BB03789C57E CRC64;

Query Match 14.7%; Score 70.5; DB 1; Length 94;
Best Local Similarity 23.7%; Pred.No. 1.8;
Matches 22; Conservative 21; Mismatches 33; Indels 17; Gaps 3;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAA---WGGSGSEAYQG----- 53
DB 5 YQFGVDVDAHGMIRAQAGSLEA---EHQAIIISDLTASDFWGGAGSAAQCGFTTQIGRNF 61
QY 54 --VQKWDATATLNNALONLARTISEAQMA 84
DB 62 QVIYEQANAHGQKQVQAAGNNMAQTDSAVGSSWA 94

RESULT 16
ES65_MYCTU STANDARD; PRT; 94 AA.
AC O53942;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ESAT-6 like protein 5.
GN RV1793 OR MT1842 OR MTV049.15.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
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RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Taylor K.,
RA Sulston J.E., Taylor K., Whitehead S., Whitehead S., Whitehead S.,
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL022021; CA917714.1; -
DR EMBL; AE007043; AAK46113.1; -
DR PIR; B70930; B70930.
DR TIGR; MT1842; -
DR Tuberculist; Rv1793; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 9942 MW; 1B7AB4913129C8D8 CRC64;

Query Match 14.7%; Score 70.5; DB 1; Length 94;
Best Local Similarity 25.5%; Pred. No. 1.8;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLLDEGKQSLTK--LAAA--WGGSGSEA----- 50
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5 YQFGVDVDAHGMIRAAQAS-----LEAEHQAIVRDLVLAAGDFWGGAGSVACQEFITQLGRN 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 51 YQGVQKQWDATATLNNALQNLAARTISEAGQAMA 84
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 FQVIYEQANAHGQKQVQAAGNNMAQTD SAVGSSWA 94
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 17
ES66 MYCTU STANDARD; PRT; 94 AA.
AC P95242;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative ESAT-6 like protein 6.
GN RV2346C OR MT2411 OR MTCY98.15C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Taylor K.,
RA Sulston J.E., Taylor K., Whitehead S., Whitehead S., Whitehead S.,

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RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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CC -----
DR EMBL; Z83860; CAB06161.1; -
DR EMBL; AE007081; AAK46704.1; -
DR PIR; C70662; C70662.
DR TIGR; MT2411; -
DR Tuberculist; Rv2346C; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 94 AA; 9954 MW; C740622D0BB7C8CA CRC64;

Query Match 14.7%; Score 70.5; DB 1; Length 94;
Best Local Similarity 25.5%; Pred. No. 1.8;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLLDEGKQSLTK--LAAA--WGGSGSEA----- 50
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 5 YQFGVDVDAHGMIRAAQA---GLLEAEHQAIVRDLVLAAGDFWGGAGSVACQEFITQLGRN 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 51 YQGVQKQWDATATLNNALQNLAARTISEAGQAMA 84
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 FQVIYEQANAHGQKQVQAAGNNMAQTD SAVGSSWA 94
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 18
CSMC_CHLVI STANDARD; PRT; 139 AA.
ID CSMC_CHLVI
AC Q46466;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Chlorosome protein C (14 kDa chlorosome protein).
GN CSMC.
OS Chlorobium vibrioforme.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8327D;
RA Chung S., Frank G., Zuber H., Bryant D.A.;
RT "Genes encoding two chlorosome components from the green sulfur
RT bacteria Chlorobium vibrioforme strain 8327D and Chlorobium
RT tepidum."
RL Photosyn. Res. 41:261-275 (1994).
CC -!- SUBCELLULAR LOCATION: Chlorosome.
CC -----
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CC -----
DR EMBL; U09867; AAA18795.1; -
KW Photosynthesis; Bacteriochlorophyll; Chlorosome.
SQ SEQUENCE 139 AA; 14102 MW; A7B6F1376A342C9E CRC64;

Query Match 14.7%; Score 70.5; DB 1; Length 139;
Best Local Similarity 19.4%; Pred. No. 2.8;
Matches 21; Conservative 20; Mismatches 48; Indels 19; Gaps 2;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAGWGGSG-----47

DB 30 LTGSAIVGGLEAGSVVETVAGTVGSLVD-----ASGIGNMIGSGGVGETIDRVAIT 84

QY 48 -SEAYQGVQCKWDATATINNALONLARTISEAGQAMASTEGNTGMF 94

DB 85 VKDVSRSAGDLYNDVRNVENVGNAAKAVGDAGSSASDAVNKIAGSF 132

RESULT 19

ID MRP4 STRPY STANDARD; PRT; 388 AA.
AC P30141;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen- and Ig-binding protein precursor (MRP protein).
GN MRP4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP4 / Serotype M4;
RX MEDLINE=92269579; PubMed=1598817;
RA Stenberg L., O'Toole P., Lindahl G.;
RT "Many group A streptococcal strains express two different
RT immunoglobulin-binding proteins, encoded by closely linked genes:
RT characterization of the proteins expressed by four strains of
RT different M-type."
RL Mol. Microbiol. 6:1185-1194 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AP4 / Serotype M4;
RX MEDLINE=92409576; PubMed=1528877;
RA O'Toole P., Stenberg L., Rissler M., Lindahl G.;
RT "Two major classes in the M protein family in group A streptococci."
RL Proc. Natl. Acad. Sci. U.S.A. 89:8661-8665 (1992).
CC -!- FUNCTION: BINDS IGG MOLECULES OF THE IGI, IG2 AND IG4 SUBCLASSES,
CC AND ALSO BINDS FIBRINOGEN.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (potential).
CC

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CC -----
DR EMBL; M87831; AAA26930.1; -
DR InterPro; IPR005877; Gpos_Y5IRK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; Y5IRK signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs; TIGR01168; Y5IRK signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.

KW IgG-binding protein; Cell wall; Peptidoglycan-anchor; Repeat; Signal.
FT SIGNAL 1 41
FT CHAIN 42 357 FIBRINOGEN- AND IG-BINDING PROTEIN.
FT PROPEP 358 388 REMOVED BY SORTASE (POTENTIAL).
FT SITE 354 358 LPXTG SORTING SIGNAL (POTENTIAL).
FT MOD RES 357 357 AMIDE-LINKED TO CELL WALL (POTENTIAL).
SQ SEQUENCE 388 AA; 42244 MW; 3AB19E8B6CEDA722 CRC64;

Query Match 14.7%; Score 70.5; DB 1; Length 388;

Best Local Similarity 23.3%; Pred. No. 9.1;
Matches 20; Conservative 20; Mismatches 41; Indels 5; Gaps 1;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEKQSLTKLAAGWGGSGSEATGVQCKWDA 60

DB 203 LTLEQAKLDTAEAKAKLESQVTTLENLGSAKRELTDQAKLDAANAE-----KEKQOS 257

QY 61 TATELNALONLARTISEAGQAMAST 86

DB 258 QAATLEKQLEATKKELADLOAKLAAT 283

RESULT 20

ID FAS1 SCHPO STANDARD; PRT; 2073 AA.
AC Q9UDG0; P78799;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fatty acid synthase subunit beta (EC 2.3.1.86) [Includes: 3-
DE hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61);
DE Enoyl-[acyl-carrier-protein] reductase (NADH) (EC 1.3.1.9); [Acyl-
DE carrier-protein] acetyltransferase (EC 2.3.1.38); [Acyl-carrier-
DE protein] malonyltransferase (EC 2.3.1.39); S-acyl fatty acid synthase
DE thioesterase (EC 3.1.2.14)].
GN FAS1 OR SPAC926.09C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A., AND SUBUNIT.
RX MEDLINE=98359895; PubMed=9693066;
RA Niwa H., Katayama E., Yanagida M., Morikawa K.;
RT "Cloning of the fatty acid synthetase beta subunit from fission yeast,
RT coexpression with the alpha subunit, and purification of the intact
RT multifunctional enzyme complex."
RL Protein Expr. Purif. 13:403-413 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy J., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.J., Warren T., Whitehead S.,
RA Woodward J., Volckart G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Db 135 ALIGQTKFHGSALLDE---SSVKLAAIFGQGYYEDFELIELYEVYAPFAEELIQVLS 191

Qy 71 NIANTISEAGQA 82
| : | : ||
Db 192 KHLFTLSQNEQA 203

RESULT 21
ES6D_MYCTU
ID_ESGD_MYCTU STANDARD; PRG; 103 AA.
AC_O05440;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative ESAT-6 like protein I3.
GN RV3905C OR MT4024 OR MTCYI5F10.06.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmier K., Gas S., Barry C.E. III, Tekalia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feldwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter A., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ESAT6 FAMILY.
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CC -----
CC EMBL; Z94121; CAB08096.1; --
DR EMBL; AR007193; AAK48388.1; --
DR EIR; B70600; B70600.
DR TIGR; MT4024; --
DR Tuberculist; RV3905c; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 103 AA, 10460 MW; 3994E27A7EDDF02 CRC64;

Query Match 14.6%; Score 70; DB 1; Length 103;
Best Local Similarity 24.1%; Pred. No. 2.2;
Matches 19; Conservative 13; Mismatches 47; Indels 0; Gaps 0;
Qy 9 AGIEAASAIQGVNTSIHSLLDEGGKSLTKLAAAGGSGSEAYQGVQQWDATA TELNNA 68
Db 12 AVMCGFAASLDGAABHLAVQLAEALDAQVGQMGLGWRGASGSYAWELWHRGAGEVOLG 71
Qy 69 LONARTISEAGCAWASTE 87

Db 72 LSLMAAIAHAGAGYQHNE 90

RESULT 22

VATI METMA
ID VATI METMA STANDARD; PRT; 649 AA.
AC OS9659;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
GN ATP OR AHA1 OR MM0785.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RA Ruppert C., Wimmers S., Mueller V.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=21210827; PubMed=1215824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boencke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
CC H(+) (out).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U47274; AAC06381.1;
CC EMBL; AE013304; AAM30481.1; ALT_INIT.
CC PIR; T45102; T45102.
CC InterPro; IPR002490; V ATPase_sub116.
CC Pfam; PF01496; V ATPase sub a; 1.
CC Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
CC
CC TRANSMEM 348 368 POTENTIAL.
FT TRANSMEM 391 411 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 458 478 POTENTIAL.
FT TRANSMEM 498 518 POTENTIAL.
FT TRANSMEM 519 539 POTENTIAL.
FT TRANSMEM 558 578 POTENTIAL.
FT TRANSMEM 592 612 POTENTIAL.
FT TRANSMEM 594 594 A -> R (IN REF. 1).
FT CONFLICT 594 594
SQ SEQUENCE 649 AA; 71963 MW; 5C1D02B67B85CAE4 CRC64;

Query Match 14.6%; Score 70; DB 1; Length 649;
Best Local Similarity 30.3%; Pred. No. 19;
Matches 20; Conservative 12; Mismatches 34; Indels 0; Gaps 0;
QY 30 DEKQSLTKLAAAGGSGAYGVQVKWDATATLNNALQNLARTISEAGQMASTEGN 89
Db 54 EEVSKVLKIRSIANYLIGIESKPPVQKSDAVLRDLDTKLINELDRITISAKTETISUENE 113

QY 90 VTGMFA 95
Db 114 LKOLDA 119

RESULT 23

IPAC SHIDY
ID IPAC SHIDY STANDARD; PRT; 382 AA.
AC Q03946;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 42 kDa membrane antigen precursor.
GN IPAC.
OS Shigella dysenteriae.
OG Flagellid invasion.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
EN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CG097;
RX MEDLINE=92114800; PubMed=1766387;
RA Yao R., Palchaudhuri S.;
RT "Nucleotide sequence of the ipaBCD structural genes of Shigella
dysenteriae."
RL Mol. Microbiol. 5:2217-2221 (1991).
CC -!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC
CC EPITHELIAL CELLS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X60777; CAA43191.1;
CC PIR; S15578; S15578.
CC InterPro; IPR005427; BacInvasinC.
CC PRINTS; PR01608; BACINVASIN.
CC Antigen; Plasmid; Virulence; Membrane; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 382 42 kDa MEMBRANE ANTIGEN.
FT SEQUENCE 382 AA; 41098 MW; A22E1D6399EC30BF CRC64;
SQ

Query Match 14.5%; Score 69.5; DB 1; Length 382;
Best Local Similarity 24.5%; Pred. No. 11;
Matches 23; Conservative 19; Mismatches 41; Indels 11; Gaps 3;
QY 3 EQQWNPAGIEAAASAIQGNVTS---IHSLLDEGKSLTKLAAAGGSGSGSEAYGVQVKW 58
Db 292 QOKQNGRATMETSVAAGNISTGGRYASALBEEELISQASSK---QAEASQVSKFAS 348

QY 59 DATATELNALQNLARTISEAGQMASTEGNVGTG 92
Db 349 QAT---NQLIQKLINIDINQSRSTASQIAG 378

RESULT 24

GUB_BACCI
ID GUB_BACCI STANDARD; PRT; 409 AA.
AC P19254;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Beta-glucanase precursor (EC 3.2.1.73) (Endo-beta-1,3-1,4 glucanase).
GN BGC
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=WL-12;
RX MEDLINE=90332423; PubMed=2377467;
RA Bueno A., Vasquez de Aldana C.R., Correa J., del Rey F.;
RT "Nucleotide sequence of a 1,3-1,4-beta-glucanase-encoding gene in
RL Bacillus circulans WL-12.";
CC Nucleic Acids Res. 18:4248-4248(1990).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glycosidic linkages
CC in beta-D-glucans containing 1,3- and 1,4-bonds.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY D (FAMILY 8 OF GLYCOSYL
CC HYDROLASES).
CC
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CC
CC EMBL; X52880; CAA37062.1; -.
CC PIR; S10485; S10485.
CC HSSP; P04955; ICSE.
CC InterPro; IPR002037; Glyco hydro 8.
CC Pfam; PF01270; Glyco hydro 8; 1.
CC PRINTS; PR00735; GLHYDRLASE8.
CC PROSITE; PS00812; GLYCOSYL_HYDROL_F8; 1.
CC Hydrolase; Glycosidase; Signal.
CC SIGNAL 1 31
CC CHAIN 32 409
CC ACT SITE 95 95
CC ACT SITE 156 156
CC ACT SITE 156 156
CC SEQUENCE 409 AA; 44816 MW; C75612167D13E76 CRC64;
CC
CC Query Match 14.2%; Score 68; DB 1; Length 409;
CC Best Local Similarity 38.8%; Pred. No. 17;
CC Matches 19; Conservative 5; Mismatches 17; Indels 8; Gaps 1;
CC
CC QY 3 EQWNFAQIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAWGGSGSEAY 51
CC Db 140 KNSFSQNFEGADSGDMDIAYSLIAKQ-----WGSGGSINY 180
CC
CC RESULT 25
CC CUG1_HUMAN
CC ID CUG1_HUMAN STANDARD; PRT; 486 AA.
CC AC Q92879; Q9NP83; Q9NR06;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE CUG triplet repeat RNA-binding protein 1 (CUG-BP1) (RNA-binding
CC protein BRUNOL-2) (deadenylation factor CUG-BP) (50 kDa Nuclear
CC polyadenylated RNA-binding protein) (EDEN-BP).
CC GN CUGBP1 OR BRUNOL2 OR CUGBP OR NAB50.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Carnivora; Hominiidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
CC RX MEDLINE=97105883; PubMed=8948631;
CC RA Timchenko L.T., Miller J.W., Timchenko N.A., DeVore D.R., Datar K.V.,
CC Lin L., Roberts R., Caskey C.T., Swanson M.S.;
CC RT "Identification of a (CUG)n triplet repeat RNA-binding protein and its
CC expression in myotonic dystrophy."
CC RL Nucleic Acids Res. 24:4407-4414(1996).
CC RN [2]
CC RP SEQUENCE FROM N.A. (ISOFORM 1).
CC RX MEDLINE=20435814; PubMed=10893231;
CC RA Good P.J., Chen Q., Warner S.J., Herring D.C.;
CC RT "A family of human RNA-binding proteins related to the Drosophila
CC Bruno translational regulator."
CC RL J. Biol. Chem. 275:28583-28592(2000).

```

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RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RP TISSUE=Brain, and Skeletal muscle;
RC Takahashi N., Sasagawa N., Usuki F., Kawahara H., Sorimachi H.,
RA Maeda T., Suzuki K., Ishiura S.;
RT "The CUG-binding protein exists in multiple isoforms and reduces DM
RL protein kinase expression."
CC Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC [4]
CC SEQUENCE FROM N.A. (ISOFORM 1).
CC RA Pailard L., Legagneux V., Osborne B.;
CC RT "EDEN-BP/CUG-BP is a highly conserved deadenylation factor involved in
CC the post-translational regulation of c-jun proto-oncogene."
CC RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC [5]
CC CHARACTERIZATION.
CC EX MEDLINE=20007898; PubMed=10536163;
CC RA Timchenko N.A., Welm A.L., Lu X., Timchenko L.T.;
CC RT "CUG repeat binding protein (CUGBP1) interacts with the 5' region of
CC C/EBPbeta mRNA and regulates translation of C/EBPbeta isoforms."
CC RL Nucleic Acids Res. 27:4517-4525(1999).
CC [6]
CC CHARACTERIZATION.
CC RP MEDLINE=21269330; PubMed=11124939;
CC RX Timchenko N.A., Cai Z.J., Welm A.L., Reddy S., Ashizawa T.,
CC RA Timchenko L.T.;
CC RT "RNA CUG repeats sequester CUGBP1 and alter protein levels and
CC activity of CUGBP1."
CC RL J. Biol. Chem. 276:7820-7826(2001).
CC -!- FUNCTION: Regulates splicing and translation of various RNAs.
CC Binds to (CUG)n triplet repeats and to Bruno response elements.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Lx1Q;
CC IsoId=Q92879-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q92879-2; Sequence=VSP_005784;
CC Name=3; Synonyms=A;
CC IsoId=Q92879-3; Sequence=VSP_005784, VSP_005785;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- DISEASE: CUGBP1 may be involved in the mechanism of myotonic
CC dystrophy. It binds to the CUG repeat expansion of the CC
CC untranslated region of the myotonin protein kinase (Mt-PK) gene.
CC -!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC
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CC
CC EMBL; U63289; AAC50895.1; -.
CC EMBL; AF248648; AAF86230.1; -.
CC EMBL; AF267533; AAF78955.1; -.
CC EMBL; AF267534; AAF78956.1; -.
CC EMBL; A0007988; CAC20566.1; -.
CC HSSP; P09651; 1HAI.
CC Genes; HGNC:2549; CUGBP1.
CC GK; Q92879; -.
CC MIM; 601074; -.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003723; F:RNA binding activity; TAS.
CC GO; GO:0006397; P:mRNA processing; TAS.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF00076; rrm; 3.
CC SMART; SM00360; RRM; 3.
CC PROSITE; PS0102; RRM; 3.
CC PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
CC mRNA processing; RNA-binding; Repeat; Nuclear protein;
CC Alternative splicing.

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FT	DOMAIN	16	99	RNA-BINDING (RRM) 1.	RA
FT	DOMAIN	108	188	RNA-BINDING (RRM) 2.	RA
FT	DOMAIN	287	308	SER-RICH.	RA
FT	DOMAIN	401	479	RNA-BINDING (RRM) 3.	RA
FT	VARSPPLIC	231	234	Missing (in isoform 2 and isoform 3).	RA
FT	VARSPPLIC	297	297	/FTId=VSP_005784.	RA
FT	VARSPPLIC	297	297	S -> SA (in isoform 3).	RA
FT	VARSPPLIC	297	297	/FTId=VSP_005785.	RA
SQ	SEQUENCE	486 AA;	52063 MW;	C4C13D77273A01D CRC64;	RA
Query Match					RA
Best Local Similarity					RA
Matches 34; Conservative					RA
Score 68; DB 1; Length 486;					RA
Pred. No. 21;					RA
Mismatches 40; Indels 60; Gaps 4;					RA
Qy	4	QOWNPAGIEAAASATQGNVTSHSLDEGKQ	34		RA
Db	260	QLQNLAAALAAASAAQNPSTGNTALTTSSPLSVLTSSGSPSSSSNVNPIASLGALQ	319		RA
Qy	35	-----SLTKLAARAGSGS-----EAYGVQCKWDATATLNN	67		RA
Db	320	TLAGATAGINVGSLAGMAALNGGLSGLSNGTGTMEALTQAYSGIQYAAAAALPTLYN	379		RA
Qy	68	ALQNL--ARTISEAGQAMASTEg 88			RA
Db	380	--QNLTOOSIGAAGSGEGPEG 400			RA
RESULT 26					RA
ID	CUG1 MOUSE	STANDARD;	PRT;	486 AA.	RA
AC	P28659; Q9CXES; Q9ERJ8; Q9J137;				RA
DT	01-DEC-1992 (Rel. 24, Created)				RA
DT	15-OCT-2001 (Rel. 40, Last sequence update)				RA
DE	CUG triplet repeat RNA-binding protein 1 (CUG-BP1) (RNA-binding				RA
DE	protein BRUNO1-2) (Deadenylation factor CUG-BP) (Deadenylation factor				RA
DE	EDEN-BP) (Brain protein F41).				RA
GN	CUGBP1 OR BRUNO12 OR CUGBP.				RA
OS	Mus musculus (Mouse).				RA
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				RA
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				RA
OX	NCBI_TaxID=10090;				RA
RN	[1]				RA
RP	SEQUENCE FROM N.A. (ISOFORM 1).				RA
RC	STRAIN=Swiss; TISSUE=Ovary;				RA
RA	Faillard L., Legagneux V., Osborne B.;				RA
RT	"EDEN-BP/CUG-BP is a highly conserved deadenylation factor involved in				RA
RT	the post-translational regulation of c-jun proto-oncogene."				RA
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				RA
RN	[2]				RA
RP	SEQUENCE FROM N.A. (ISOFORM 1).				RA
RC	TISSUE=Liver;				RA
RA	Takahashi N., Sasagawa N., Usuki F., Kawahara H., Sorimachi H.,				RA
RA	Maeda T., Suzuki K., Ishiura S.;				RA
RT	"The CUG-binding protein exists in multiple isoforms and reduces DM				RA
RT	protein kinase expression."				RA
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.				RA
RN	[3]				RA
RP	SEQUENCE FROM N.A. (ISOFORM 3).				RA
RC	STRAIN=C57BL/6J; TISSUE=Embryonic liver;				RA
RX	MEDLINE=21085660; PubMed=11217851;				RA
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				RA
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				RA
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,				RA
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				RA
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				RA
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				RA
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,				RA
RA	Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				RA
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Baren G.,				RA
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				RA
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				RA
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				RA

RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				RA
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				RA
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				RA
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				RA
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,				RA
RA	Hayashizaki Y.;				RA
RT	"Functional annotation of a full-length mouse cDNA collection."				RA
RL	Nature 409:685-690(2001).				RA
RN	[4]				RA
RP	SEQUENCE OF 127-445 FROM N.A. (ISOFORM 1).				RA
RC	Kato K.;				RA
RA	Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.				RA
CC	!- FUNCTION: Regulates splicing and translation of various RNAs.				RA
CC	Binds to (CUG)n triplet repeats and to Bruno response elements (By				RA
CC	similarity).				RA
CC	!- SUBCELLULAR LOCATION: Nuclear (By similarity).				RA
CC	!- ALTERNATIVE PRODUCTS:				RA
CC	Event=Alternative splicing; Named isoforms=3;				RA
CC	Comment=Experimental confirmation may be lacking for some				RA
CC	isoforms;				RA
CC	Name=1; Synonyms=LVIQ;				RA
CC	Isoid=P28659-1; Sequence=Displayed;				RA
CC	Name=2;				RA
CC	Isoid=P28659-2; Sequence=VSP_005786;				RA
CC	Name=3; Synonyms=A;				RA
CC	Isoid=P28659-3; Sequence=VSP_005787;				RA
CC	!- TISSUE SPECIFICITY: NEOCORTEX, CEREBELLAR CORTEX, HIPPOCAMPUS AND				RA
CC	OTHER AREAS, ABUNDANT IN THE PUTAMEN, AND POORLY EXPRESSED IN THE				RA
CC	THALAMUS AND IN THE BRAIN STEM.				RA
CC	!- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.				RA
CC	!- CAUTION: Ref.4 sequence differs from that shown due to a				RA
CC	frameshift in position 367.				RA
CC	-----				RA
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				RA
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CC	use by non-profit institutions as long as its content is in no way				RA
CC	modified and this statement is not removed. Usage by and for commercial				RA
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				RA
CC	or send an email to license@isb-sib.ch).				RA
CC	-----				RA
DR	EMBL; AJ7007987; CAC20707.1; -				RA
DR	EMBL; AF2675535; AAF78957.1; -				RA
DR	EMBL; AK014492; BAB29392.1; -				RA
DR	EMBL; X61451; CAA43691.1; ALT_FRAME.				RA
DR	MCD; MGI:1342295; Cudbpl.				RA
DR	GO; GO:0008248; F:pre-mRNA splicing factor activity; IDA.				RA
DR	GO; GO:0006376; P:pre-mRNA splice site selection; IDA.				RA
DR	InterPro; IPR000504; RNA_rec_mot.				RA
DR	Pfam; PF00076; rrm; 3.				RA
DR	PROSITE; PS50102; RRM; 3.				RA
DR	PROSITE; PS00030; RRM_RNP_1; FALSE NEG.				RA
KW	mRNA processing; RNA-binding; Repeat; Nuclear protein;				RA
KW	Alternative splicing.				RA
FT	DOMAIN	16	99	RNA-BINDING (RRM) 1.	RA
FT	DOMAIN	108	188	RNA-BINDING (RRM) 2.	RA
FT	DOMAIN	287	308	SER-RICH.	RA
FT	DOMAIN	401	479	RNA-BINDING (RRM) 3.	RA
FT	VARSPPLIC	231	234	Missing (in isoform 2 and isoform 3).	RA
FT	VARSPPLIC	297	297	/FTId=VSP_005786.	RA
FT	VARSPPLIC	297	297	S -> SA (in isoform 3).	RA
FT	VARSPPLIC	297	297	/FTId=VSP_005787.	RA
FT	CONFLICT	291	291	L -> P (IN REF. 2).	RA
FT	CONFLICT	301	301	P -> T (IN REF. 2).	RA
FT	CONFLICT	335	335	G -> R (IN REF. 2).	RA
FT	CONFLICT	347	347	G -> A (IN REF. 2).	RA
SQ	SEQUENCE	486 AA;	52107 MW;	ABE22D331A62B584 CRC64;	RA
Query Match					RA
Best Local Similarity					RA
Matches 34; Conservative					RA
Score 68; DB 1; Length 486;					RA
Pred. No. 21;					RA
Mismatches 40; Indels 60; Gaps 4;					RA
Qy	4	QOWNPAGIEAAASATQGNVTSHSLDEGKQ	34		RA

RA Tse W.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,
RA Gwynn B., Peters L.B., Lux S.B.;
RT "A new spectrin, beta-IV, has a major truncated isoform that
RT associates with promyelocytic leukemia protein nuclear bodies and the
RT nuclear matrix.";
RL J. Biol. Chem. 276:23974-23985(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=20539976; PubMed=11086001;
RA Berghs S., Aguijaro D., Dirx R. Jr., Maksimova E., Stabach P.,
RA Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort T.,
RA Solimena M.;
RA "Betalv spectrin, a new spectrin localized at axon initial segments
RT and nodes of ranvier in the central and peripheral nervous system.";
RL J. Cell Biol. 151:985-1002(2000).
RN [3]
RP SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RA MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
CC -!- ALTERNATIVE PRODUCTS.
CC Event-Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H254-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H254-2; Sequence=VSP_000725, VSP_000726;
CC Name=3;
CC IsoId=Q9H254-3; Sequence=VSP_000723, VSP_000724;
CC Name=4;
CC IsoId=Q9H254-4; Sequence=VSP_000727, VSP_000728;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
CC islets.
CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 18 spectrin repeats.
CC -----
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CC -----
DR EMBL; AF311855; AAG42473.1; -;
DR EMBL; AF082075; AAG38874.1; -;
DR EMBL; AY004226; AAF93171.1; -;
DR EMBL; AY004226; AAF93172.1; -;
DR EMBL; AY004227; AAF93173.1; -;
DR EMBL; AB046862; BAB13468.1; -;
DR HSSP; Q01082; hskr.
DR Genbank; HGNC:14896; SPTEN4.
DR MIM; 606214; -;
DR GO; GO:0016363; C:nuclear matrix; IDA.
DR GO; GO:0016605; C:PML body; IDA.
DR GO; GO:0008091; C:spectrin; IDA.
DR GO; GO:0003779; F:actin binding activity; TAS.
DR GO; GO:0030506; F:ankyrin binding activity; IDA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR GO; GO:0007016; P:cytoskeletal anchoring; TAS.
DR GO; GO:0016192; P:vesicle-mediated transport; TAS.
DR InterPro; IPR001589; Actbind actnin.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001605; Spectrin_PH.
DR Pfam; PF00307; CH; 2.
DR Pfam; PF00169; PH; 1.

DR Pfam; PF00435; spectrin; 18.
DR PRINTS; PR00683; SPECTRINPH.
DR SMART; SMO0033; CH; 2.
DR SMART; SMO0233; PH; 1.
DR SMART; SMO0150; SPEC; 16.
DR DR PROSITE; PS00019; ACTININ_1; 1.
DR DR PROSITE; PS00020; ACTININ_2; 1.
DR DR PROSITE; PS00021; CH; 2.
DR DR PROSITE; PS00003; PH DOMAIN; 1.
KW Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
KW Alternative splicing.
FT DOMAIN 1 282 ACTIN-BINDING (BY SIMILARITY).
FT CH 1.
FT CH 2.
FT SPECTRIN 1.
FT SPECTRIN 2.
FT SPECTRIN 3.
FT SPECTRIN 4.
FT SPECTRIN 5.
FT SPECTRIN 6.
FT SPECTRIN 7.
FT SPECTRIN 8.
FT SPECTRIN 9.
FT SPECTRIN 10.
FT SPECTRIN 11.
FT SPECTRIN 12.
FT SPECTRIN 13.
FT SPECTRIN 14.
FT SPECTRIN 15.
FT SPECTRIN 16.
FT SPECTRIN 17.
FT SPECTRIN 18.
FT PH.
FT Missing (in isoform 3).
FT FTID=VSP_000723.
FT AVAAEGLRQNIYGEQAEVTRLEK -> MHPVPSCS
FT SAPSGTPIPPQIQLEAHR (in isoform 3).
FT FTID=VSP_000724.
FT NOENLRAQQWQKLDQLELQH -> CLIIHPALHPWE
FT PVLPRSS (in isoform 2).
FT FTID=VSP_000725.
FT Missing (in isoform 2).
FT FTID=VSP_000726.
FT IBKIAEQSQPTPLLGKRFQDPTTELAAKAAPLPPGY
FT E -> PRREDHLPNGVDQDPWQHTKPSLPKPKANKEKTAR
FT RGTCL (in isoform 4).
FT FTID=VSP_000727.
FT Missing (in isoform 4).
FT FTID=VSP_000728.
FT MISSING (IN REF. 2).
FT L -> S (IN REF. 2).
FT E -> K (IN REF. 2).
FT E -> K (IN REF. 2).
FT G -> S (IN REF. 1).
FT S
SQ SEQUENCE 2564 AA; 288982 MW; 52CDE7D11D601ECC CRC64;
Query Match 14.2%; Score 68; DB 1; Length 2564;
Best Local Similarity 26.2%; Pred. No. 1.4e+02;
Matches 21; Conservative 16; Mismatches 29; Indels 14; Gaps 4;
QY 5 QWNFAGIEAASAIQGNVTSIHSLDREGKSLTKLAAAGSGSSEAYQGVQ---KWDAT 61
DB 1021 QWRLSGIEALQALEPQA---ALLBEA---ALLAERFPAQAARLHQGAELGAEWGAL 1073
QY 62 ATELNALQNLARTISEAQ 81
DB 1074 A-----SAAQACGEAVAAAGR 1089
RESULT 23
FLIC_SHIFL STANDARD; PRT; 550 AA.
ID FLIC_SHIFL
AC Q08860;


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FT REPEAT 1032 1037 12.
FT REPEAT 1043 1048 13.
FT REPEAT 1052 1057 14.
FT REPEAT 1058 1063 15.
SQ SEQUENCE 1063 AA; 115649 MW; E4324DB6B1E4721A CRC64;

Query Match
Best Local Similarity 14.0%; Score 67; DB 1; Length 1063;
Matches 28; Conservative 9; Mismatches 43; Indels 48; Gaps 3;

QY 9 AGIEAASAIQGNVTSIHSLIDEGKQSLTKL----- 39
Db 891 AGAATSSGLSGMTFGWSSFDGKTPAVNAHGGGGVSSWGGASTWGGQNGGASAW 950
QY 40 -----AAAWGGSGSEAYQ-----GVQOKWDATAT-----ELNNALQNIARTISEAG 80
Db 951 GGAGGGASAWGGQCTGATSTWGGASAWGNKSSWGGASTWASGGSNGAMSTWGGTGDRSA 1010
QY 81 QAMASTEg 88
Db 1011 YGGASTWG 1018
```

Search completed: February 5, 2004, 17:38:48
Job time : 7.52381 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:34:22 ; Search time 13.7976 Seconds
(without alignments)
1776.756 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQQWNPAGTEAAASATQ.....ISEAGQWASTEGNVTGMFA 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830521

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database :

SPTREMBL 23 : *
1: sp archaea : *
2: sp bacteria : *
3: sp fungi : *
4: sp human : *
5: sp invertebrate : *
6: sp mammal : *
7: sp mhc : *
8: sp organelle : *
9: sp phage : *
10: sp plant : *
11: sp rodent : *
12: sp virus : *
13: sp vertebrate : *
14: sp unclassified : *
15: sp rvirus : *
16: sp bacteriophage : *
17: sp archaea : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	151	31.5	96	16	Q8NST7
2	150	31.3	96	16	Q8FS23
3	103	21.5	96	16	Q8G878
4	91	19.0	1460	16	Q8K6B1
5	86.5	18.1	100	16	O05261
6	84	17.5	142	10	Q8H0Q4
7	81.5	17.0	108	16	Q8NST8
8	79	16.5	104	16	Q9CCV7
9	77.5	16.2	135	16	O06262
10	77	16.1	876	16	Q8G727
11	76.5	16.0	903	2	Q8VTF1
12	76.5	16.0	9904	16	Q8NWQ6
13	75.5	15.8	106	16	Q8FS24
14	75.5	15.8	305	10	Q9LLS8
15	75	15.7	490	16	Q8HXZ9
16	75	15.7	1037	16	Q8XEh2

17	75	15.7	1037	16	Q8FF84
18	74.5	15.6	186	5	Q17179
19	73.5	15.3	186	5	Q17180
20	73.5	15.3	331	10	Q8S9Q2
21	73.5	15.3	371	16	Q97M89
22	73.5	15.3	389	2	Q92IX5
23	73.5	15.3	772	16	Q8E2M9
24	73.5	15.3	772	16	Q8DW39
25	73.5	15.3	2785	16	Q8EXW6
26	73.5	15.3	3141	16	Q8F850
27	73	15.2	760	5	Q96H0H
28	73	15.2	1204	16	Q915S5
29	73	15.2	2470	5	Q9VK45
30	72.5	15.1	238	10	Q49013
31	72.5	15.1	344	12	Q91BA2
32	72.5	15.1	501	13	Q91BD0
33	72.5	15.1	756	2	Q44102
34	72	15.0	96	16	Q9KE84
35	72	15.0	637	16	Q9AAK8
36	72	15.0	1225	16	Q9RZ46
37	72	15.0	4631	4	Q8WY2
38	72	15.0	5938	4	Q96PK2
39	72	15.0	6713	16	Q99U54
40	72	15.0	6713	16	Q931R6
41	71.5	14.9	526	16	Q9RUB1
42	71.5	14.9	927	16	Q928S2
43	71	14.8	97	16	Q97M29
44	71	14.8	185	13	Q8UJ68
45	71	14.8	334	10	Q9XEN7
46	71	14.8	415	2	P95813
47	71	14.8	896	16	Q8PAJ6
48	70.5	14.7	425	2	Q54860
49	70.5	14.7	485	9	Q8SCI0
50	70.5	14.7	656	16	Q9WYR0
51	70.5	14.7	656	16	Q9WXN0
52	70.5	14.7	661	16	Q9X020
53	70.5	14.7	957	10	Q94GY5
54	70.5	14.7	1510	9	O80179
55	70.5	14.7	2475	2	O82833
56	70	14.6	265	16	Q8NNM8
57	70	14.6	653	16	Q8FQL5
58	70	14.6	710	13	Q91402
59	70	14.6	1339	5	Q9VM06
60	69.5	14.5	362	16	Q9F321
61	69.5	14.5	569	16	Q8XR59
62	69.5	14.5	664	16	Q8RBV6
63	69.5	14.5	742	2	Q9X4H8
64	69.5	14.5	825	17	Q8TJH9
65	69.5	14.5	1024	10	Q9SKV4
66	69.5	14.5	1509	16	Q9SST6
67	69.5	14.5	1509	16	Q91M0
68	69.5	14.5	3165	16	Q8RDQ9
69	69	14.4	205	9	Q8LTT0
70	69	14.4	221	16	Q8NM43
71	69	14.4	222	2	Q93EL3
72	69	14.4	337	17	Q972P4
73	69	14.4	472	2	Q8GQ61
74	69	14.4	484	4	Q96RQ5
75	69	14.4	484	11	Q9R0B2
76	69	14.4	484	11	Q92187
77	69	14.4	488	4	Q96NW9
78	69	14.4	490	4	Q9UL67
79	69	14.4	508	4	Q95319
80	69	14.4	508	11	Q920H4
81	69	14.4	509	4	Q96RQ6
82	69	14.4	509	4	Q92950
83	69	14.4	521	4	Q8N499
84	69	14.4	532	11	O88756
85	69	14.4	572	16	Q92TP8
86	69	14.4	1037	16	Q8ZN77
87	69	14.4	1037	16	Q8Z4S4
88	68.5	14.3	103	16	O86644
89	68.5	14.3	138	10	Q8S386

Q8ff84 escherichia
Q17179 bombyx mori
Q17180 bombyx mori
Q8s9q2 oryza sativ
Q97m89 clostridium
Q92ix5 streptococ
Q8e2m9 streptococ
Q8dws9 streptococ
Q8exw6 streptococ
Q8f850 leptospira
Q96h0h drosophila
Q915s5 pseudomonas
Q9vk45 drosophila
Q49013 glycine max
Q91ba2 spodoptera
Q91bd0 brachydanio
Q44102 anaplasma m
Q9ke84 bacillus ha
Q9aaK8 caulobacter
Q9rZ46 deinococcus
Q8WY2 homo sapien
Q96PK2 homo sapien
Q99U54 staphylococ
Q931R6 staphylococ
Q9rub1 deinococcus
Q928S2 listeria in
Q97m29 clostridium
Q8fj68 oncorhynchu
Q9xen7 triticum ae
P95813 streptococ
Q8p4j6 xanthomonas
Q54860 streptococ
Q8sci0 propionibac
Q9WYR0 thermotoga
Q9WXN0 thermotoga
Q9X020 thermotoga
Q94GY5 oryza sativ
O80179 streptococ
O82833 bacillus sp
Q8NNM8 corynebacte
Q8fql5 corynebacte
Q91402 xenopus. he
Q9VM06 drosophila
Q9f321 streptomyce
Q8XR59 ralstonia s
Q8RBV6 thermoanaer
Q9X4H8 anaplasma m
Q8TJH9 methanosarc
Q9SKV4 arabidopsis
Q9SST6 staphylococ
Q931M0 staphylococ
Q8rdq9 fusobacteri
Q8ltt0 bacterioph
Q8nm43 corynebacte
Q93el3 borrelia bu
Q972p4 sulfolobus
Q8gq61 pseudomonas
Q96rg5 homo sapien
Q9r0b2 mus musculu
Q92187 mus musculu
Q96nw9 homo sapien
Q9ul67 homo sapien
Q95319 homo sapien
Q920h4 mus musculu
Q96rg6 homo sapien
Q92950 homo sapien
Q8n499 homo sapien
O88756 rattus norv
Q92tp8 rhizobium m
Q8zn77 salmonella
Q8z4s4 salmonella
O86644 streptomyce
Q8s386 secale cere

90 68.5 14.3 414 10 Q8RZT1 Q8RZT1 oryza sativ

ALIGNMENTS

RESULT 1

Q8NST7 ID Q8NST7 PRELIMINARY; PRT; 96 AA.
AC Q8NST7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein Cgi0580.
GN CGL0580.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005275; BAB97973.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 10324 MW; 724318FEAE03AD76 CRC64;

Query Match 31.5%; Score 151; DB 16; Length 96;
Best Local Similarity 37.5%; Pred. No. 4.7e-07;
Matches 30; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

QY 5 QWVFAGTAAATDINSTGRINSLLDGLKQQLQPMVATWEGDSAYAYNEAQMKWDNAAAA 64
Db 5 RYFEGAIQGAATDINSTGRINSLLDGLKQQLQPMVATWEGDSAYAYNEAQMKWDNAAAA 64
QY 65 LNNAQLNQLARTISEAGQAMA 84
Db 65 LNTILATISQTVSQGAERMS 84

RESULT 2

Q8FS23 ID Q8FS23 PRELIMINARY; PRT; 96 AA.
AC Q8FS23;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN CE0593.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005215; BAC17393.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 10310 MW; EF8D4BDC9E40F0A5 CRC64;

Query Match 31.3%; Score 150; DB 16; Length 96;
Best Local Similarity 37.5%; Pred. No. 5.9e-07;
Matches 30; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

QY 5 QWVFAGTAAATDINSTGRINSLLDGLKQQLQPMVATWEGDSAYAYNEAQMKWDNAAAA 64
Db 5 RYFEGAIQGAATDINSTGRINSLLDGLKQQLQPMVATWEGDSAYAYNEAQMKWDNAAAA 64

Db 5 RYFEGAIQGAATDINSTGRINSLLDGLKQQLQPMVATWEGDSAYAYNEAQMKWDNAAAA 64
QY 65 LNNAQLNQLARTISEAGQAMA 84
Db 65 LNTILATISQTVSQGAERMS 84

RESULT 3

Q8G878 ID Q8G878 PRELIMINARY; PRT; 96 AA.
AC Q8G878;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN BL0033.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RA MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karimantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014614; AAN23870.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 10431 MW; 7D02BE38C6B1F61C CRC64;

Query Match 21.5%; Score 103; DB 16; Length 96;
Best Local Similarity 22.1%; Pred. No. 0.018;
Matches 21; Conservative 29; Mismatches 45; Indels 0; Gaps 0;

QY 1 MTEQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAWGGSGSEAYQGVQKWDATA 60
Db 1 MPQYQVDSERIOSSAAVATISQIRQAVGGMYTNLALQDAWRGSAATQFTVAEOWRA 60
QY 61 TATELNNAQLNQLARTISEAGQAMASTEIGNVTGMFA 95
Db 61 AQQMEASLESQRSLSQTASTVYADAEIQASRLFA 95

RESULT 4

Q8K6B1 ID Q8K6B1 PRELIMINARY; PRT; 1460 AA.
AC Q8K6B1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative tail protein-phage associated.
GN SPYM3 1421.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=1212206;
RA Beres S.B., Syiva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus: phage-encoded toxins, the high-virulence phenotype, and clone emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
DR EMBL; AE014163; AAM80028.1; -.

DR InterPro; IPR001680; WD40.
 DR PROSITE; PS00678; WD REPEATS 1; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1460 AA; 149590 MW; 109AB8DDFBD4A4B8 CRC64;

Query Match 19.0%; Score 91; DB 16; Length 1460;
 Best Local Similarity 33.0%; Pred. No. 7.5;
 Matches 31; Conservative 13; Mismatches 42; Indels 8; Gaps 4;

QY 4 QOWN--FAGIEAASAIQGNVTSHLSLLDEGKQSLTKLAAWGGSGSEAYQGVQKWDAT 61
 DB 222 QWNFFSVSAKAFANKVST--SLFGLTSSLANLSKIGSSLS--NGFSRMSSSA 276
 QY 62 ATELNNALQNLARTISEAGQMASTEGNVTGMFA 95
 DB 277 ATSLNGISQKFANT--SSAGERLKSIVMSIVQAFS 309

RESULT 5
 ID O06261 PRELIMINARY; PRT; 100 AA.
 AC O06261;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DE Hypothetical protein RV3444C.
 GN RV3444C OR MTCY77.16C OR MT3549.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eigmler K., Gas S., Barry C.E. III, Tekala E.,
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.";
 RL Nature 393:537-544 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 Peterson J., DeBoy R., Dodson R., Winn M.L., Haft D., Hickey E.,
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 Bishai W.;
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z95389; CAB09674.1; --
 DR EMBL; AE007159; AAK47890.1; --
 DR TIGR; MT3549; --
 DR TubercuList; RV3444C; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 100 AA; 11120 MW; 5045B1B46578DC6C CRC64;

Query Match 18.1%; Score 86.5; DB 16; Length 100;
 Best Local Similarity 24.2%; Pred. No. 0.7;
 Matches 22; Conservative 13; Mismatches 55; Indels 1; Gaps 1;

QY 6 WNPAGIE-AAASAIQGNVTSHLSLLDEGKQSLTKLAAWGGSGSEAYQGVQKWDATATE 64
 DB 9 YNFDALEYSVROEIHHTAARFNAALQELRSQAPLQQLWTREAAAYHAELKQWQAASA 68
 QY 65 LNNALQNLARTISEAGQMASTEGNVTGMFA 95

Db 69 LNEILLDLGNVVRHGADDDVAHADRRAGA 99

RESULT 6
 ID Q8HQ04 PRELIMINARY; PRT; 142 AA.
 AC Q8HQ04;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DE Hypothetical protein precursor.
 GN COR14B.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Aurea;
 RA Dal Bosco C., Busconi M., Govoni C., Baldi P., Stanca M.A.,
 Crosatti C., Bassi R., Cattivelli L.;
 RT "Cor gene expression in barley mutants affected in chloroplast
 development and photosynthetic electron transport.";
 RL Plant Physiol. 0:0-0(0).
 DR EMBL; AJ512944; CAD55692.1; --
 KW Transit peptide; Chloroplast.
 FT TRANSIT 1 52 CHLOROPLAST.
 FT CHAIN 53 142 COLD REGULATED PROTEIN.
 SQ SEQUENCE 142 AA; 13919 MW; EC4860B010D59694 CRC64;

Query Match 17.5%; Score 84; DB 10; Length 142;
 Best Local Similarity 22.9%; Pred. No. 1.9;
 Matches 16; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 12 EAAASAIQGNVTSHLSLLDEGKQSLTKLAAWGGSGSEAYQGVQKWDATATELNNALQN 71
 DB 73 DATDNVAGAKSAGESVVDAAKDGASKVSETAQLDGGQAKQAEEAWDATKDAQAQSVADN 132
 QY 72 LARTISEAGQ 81
 DB 133 VAAAVEDVSK 142

RESULT 7
 ID Q8NST8 PRELIMINARY; PRT; 108 AA.
 AC Q8NST8;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE Hypothetical protein Cgl0579.
 GN CGL0579.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005275; BAB97972.1; --
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 108 AA; 11644 MW; E0B3AFA03AE9D452 CRC64;

Query Match 17.0%; Score 81.5; DB 16; Length 108;
 Best Local Similarity 18.2%; Pred. No. 2.3;
 Matches 14; Conservative 24; Mismatches 32; Indels 7; Gaps 1;

QY 18 IQGNVTSHLSLLDEGKQSLTKLAAWGGSGSEAYQGVQKWDATATELNNALQNLARTIS 77

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Ra Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Ra Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Ra Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy J.,
Ra Oliver S., Seeger K., Skelton S., Squares S., Rogers J.,
Ra Rutter S., Taylor K., Whitehead S., Barrell B.G.;
Ra Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
Ra Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Ra Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Ra Kiehl J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Ra Deichner A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Ra Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z95389; CAB08675.1; ALT INIT.
DR EMBL; AE007159; AAK47891.1; -.
DR TIGR; MT3550; -.
DR TubercuList; RV3445C; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 135 AA; 14592 MW; A6BC5AED45621C07 CRC64;

Query Match 16.2%; Score 77.5; DB 16; Length 135;
Best Local Similarity 35.3%; Pred. No. 7.4; 18; Indels 7; Gaps 1;
Matches 18; Conservative 8; Mismatches 18;

QY 41 AAWGSGSEAYGVQVQKWDATATLNNALQNLARTI-----SEAGQAMA 84
Db 75 SVWGGLAARFQDVDRWNAESTRLVHLHAADTIRHNEAALREAGQIHA 125

RESULT 10
ID Q8G727 PRELIMINARY; PRT; 876 AA.
AC Q8G727;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical membrane protein with similarity to phage infection
DE protein.
GN BL0446.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
Ra Schell M.A., Karmirantzou M., Snel B., Villanova D., Berger B.,
Ra Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
Ra Bridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014664; AAN24282.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 876 AA; 93283 MW; A5966B73BF878545 CRC64;

Query Match 16.1%; Score 77; DB 16; Length 876;
Best Local Similarity 26.7%; Pred. No. 86;
Matches 23; Conservative 18; Mismatches 33; Indels 12; Gaps 2;

QY 11 IEAASAIQGNVTSIHSLDEGKSLTKLAAAWGGS-----GSEAYGVQVQKWDAT 64
Db 412 LSSSTASTLTGTSISQGLIQSKHALQDLQDLQKAASTVTALRDTDKALAGVQTKLDTL 471
QY 65 LNNALQNLARTISEAGQAMASTEAGNV 90

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"A kernel-specific 1,3-beta glucanase in oat."; Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RT	
RL	
DS	
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KW	Complete proteome.
SQ	SEQUENCE 9904 AA; 1068476 MW; C8B6908F75EA56B2 CRC64;

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DR HSP; P15737; IGHS.
DR InterPro; IPR000490; Glyco_hydro_17.
DR Pfam; PF00332; Glyco_hydro_17; 1.
FT NON TER
SQ SEQUENCE 305 AA; 32358 MW; FEE831E77D0872EE CRC64;

Query Match 15.8%; Score 75.5; DB 10; Length 305;
Best Local Similarity 25.6%; Pred. No. 32;
Matches 31; Conservative 22; Mismatches 39; Indels 29; Gaps 5;

QY 1 MTEQOWNFAGLEAAASALQGNVTSIHSLDEGKQSLTKL-----AAAWGSGSEAYQGV 54
DB 27 ITDMRIYFADGQ-ALSALRN--SGILVMDIGNDQKGIAGSANAARWFDNVQRQGL 83
QY 55 QOKWDATATELNN-----ALQNARTISEAG-----QAMASTEGNVTGMF 94
DB 84 KIKIVAGNEIQGGDTGRIVPAIRNLNLAALSAAGLIGGKIVSTAIRFDVANSPSPAGVF 143
QY 95 A 95
DB 144 A 144

RESULT 15
Q9H2X9 PRELIMINARY; PRT; 490 AA.
AC Q9H2X9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Probable chemotaxis transducer.
GN PA2867.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AB004713; AAG06255.1; -.
DR HSP; P02942; 1QU7.
DR InterPro; IPR004089; Chmtaxis_trans.
DR Pfam; PF003660; HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCFsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
DR PROSITE; PS0111; CHEMOTAXIS_TRANSLOC_2; 1.
KW Complete proteome.
SQ SEQUENCE 490 AA; 51457 MW; 1ED660B984A963CA CRC64;

Query Match 15.7%; Score 75; DB 16; Length 490;
Best Local Similarity 29.1%; Pred. No. 64;
Matches 23; Conservative 12; Mismatches 36; Indels 8; Gaps 2;

QY 8 FAGIEAAASAIQGNVTSIHSLDEGKQSLTKLAAGWGGSEAYQGVQOKWDATATELNN 67
DB 201 FNAWQAGYQIRIVGTVAATATKLDGAQALARM-----GQVRQGMIGQSEETDQTAIN- 255
QY 68 ALQNARTISEAGQAMST 86
DB 256 ---EMSTVPHIAQHAAT 271
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RESULT 16
Q8XE2 PRELIMINARY; PRT; 1037 AA.
AC Q8XE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sensitivity to acriflavine, integral membrane protein, possible efflux
DE pump (Aminoglycoside efflux pump) (Putative transport system permease
DE protein).
DE ACRD OR Z3727 OR ECS3332.
GN Escherichia coli O157:H7.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamocousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Iida T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001)
DR EMBL; AB005476; AAG57579.1; -.
DR EMBL; AP002561; BAB36755.1; -.
DR InterPro; IPR001036; Acriflavin_res.
DR InterPro; IPR004764; HAE1.
DR Pfam; PF00873; ACR tran; 1.
DR PRINTS; PR00702; ACRIFLAVINRP.
DR TIGRFAMs; TIGR00915; 2A0602; 1.
KW Complete proteome.
FT CONFLICT 127 127 V -> L (IN REF. 2).
SQ SEQUENCE 1037 AA; 113019 MW; B44742633B1DA058 CRC64;

Query Match 15.7%; Score 75; DB 16; Length 1037;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
Matches 27; Conservative 18; Mismatches 39; Indels 20; Gaps 4;

QY 7 NFAGIEA-----AASAIQGNVTSIHSL-----DEGKQSLTKLAAGWGGSEAYQGV 53
DB 48 NYPGASQULENTVTQVIEQNNTGLDNLNMYSSQSGGTQASVT-LSFRAGTDPDEAVQ 106
QY 54 VQOKWDATATELNNALQNARTISEAGQ-----AMASTEGNV 90
DB 107 VQNLQSAQRKLPQAVQNGQVTRKTGDTNLTIAFVSTDGS 149

RESULT 17
Q8FF84 PRELIMINARY; PRT; 1037 AA.
AC Q8FF84;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable aminoglycoside efflux pump.
GN ACRD OR C2997.
OS Escherichia coli O6.
```

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX	Enterobacteriaceae; Escherichia.
OC	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=O6.H1 / CPT073 / ATCC 700928;
RX	MEDLINE=22388234; PubMed=12471157;
RA	Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA	Rasko D., Buckles E.L., Zhou S.-R., Boutin A., Hackett J., Stroud D.,
RA	Mayhew G.F., Rose D.J., Liou S., Schwartz D.C., Perna N.T.,
RA	Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT	"Extensive mosaic structure revealed by the complete genome sequence
RT	of uropathogenic Escherichia coli.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR	EMBL; AE016764; AA81447.1; --
KW	Complete proteome.
SQ	SEQUENCE 1037 AA; 113093 MW; 94CE259053DF1461 CRC64;
Query Match	15.7%; Score 75; DB 16; Length 1037;
Best Local Similarity	26.2%; Pred. No. 1.6e+02;
Matches	27; Conservative 18; Mismatches 38; Indels 20; Gaps 4;
QY	7 NFAGIEA-----AASATGQNVTSIHSLL-----DECKQSILTKLAANGSGSSEAYQG 53
Dd	: :
Db	48 NYPGASQTLENTVTQVTEQNITGLDNLIMYMSSSGTGQASVT-LSFKAQTDPDEAVQQ 106
QY	54 VQOKWDATATELNALQNLARTISFAGQ-----AMASTEGNV 90
Dd	: :
Db	107 VONQLQSARMKLPQAVQNGQTVVRKTDGTNLTIAFVSTDGSM 149
RESULT 18	
ID	Q17179 PRELIMINARY; PRT; 186 AA.
AC	Q17179;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Apolipophorin-III precursor.
OS	Bombyx mori (Silk moth).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Lepidoptera; Glossata; Diptysia; Bombycoidea;
OC	Bombycidae; Bombyx.
OX	NCBI_TaxID=7091;
OX	[1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=N4; TISSUE=Fat body;
RC	MEDLINE=20082772; PubMed=10613959;
RA	Yamauchi Y., Hoefler C., Yamamoto A., Takeda H., Ishihara R.,
RA	Maekawa H., Sato R., Su-II S., Sumida M., Wells M.A., Tsuchida K.;
RT	"cDNA and deduced amino acid sequences of apolipophorin-IIIs from
RT	Bombyx mori and Bombyx mandarina.";
RL	Arch. Insect Biochem. Physiol. 43:16-21 (2000).
DR	EMBL; U59243; AAB02852.1; --
KW	Signal.
FT	SIGNAL.
FT	CHAIN 1 22 POTENTIAL.
SQ	SEQUENCE 186 AA; 20771 MW; B5P66548C439DIBC CRC64;
Query Match	15.6%; Score 74.5; DB 5; Length 186;
Best Local Similarity	27.7%; Pred. No. 21;
Matches	33; Conservative 11; Mismatches 38; Indels 37; Gaps 5;
QY	8 FAGIEAAASA-----IQGVNTSIHSLDEGKSILTK-----LAAAWGSGSSE 49
Dd	: :
Db	9 FACISLAQGMVPRDAPDFFKOLEHTKEFHKTLEQQFNLSLKSDAQDFSKAW-KDGSE 67
QY	50 AYOGVOQRKDWTATELNAL-----QNLARTISEAGQMASNEGVTGM 93
Dd	: :
Db	68 S----VLQQLNAFAKSLQGALGDANAKAKALECSQRNIERTAEELRKHPDVKKNTAL 123
RESULT 19	

Query Match 15.3%; Score 73.5; DB 10; Length 331;
Best Local Similarity 32.9%; Pred. No. 55;
Matches 26; Conservative 13; Mismatches 27; Indels 13; Gaps 4;
QY 13 AAASAIQGNVTSIHSLDEG--KQSLTKLAAA-WGGSGSEAYQGVQKQWDTAT-- 67
DB 66 ATLRLAAG--TJIAVIVDEPAIDQLTLTSAASDWQSNIKPYQGVNIYIAGVNEVSGDA 123
QY 68 -----ALQNLTARTISEAG 80
DB 124 TRESILPAMENLTAKLSAAG 142
RESULT 21
ID Q97M89 PRELIMINARY; PRT; 371 AA.
AC Q97M89;
DT 01-OCT-2001 (TREMELrel. 18, Created)
DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Cell wall-associated hydrolase.
GN CAC0309.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Bretton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatunov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
RA "Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum";
RT J. Bacteriol. 183:4823-4838 (2001).
RL EMBL; AEO07545; AAK78290.1; -
DR InterPro; IPR000064; NLP_C60.
DR Pfam; PF00877; NLP_C60; 1.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 371 AA; 41319 MW; B817536899C7EB8A CRC64;
Query Match 15.3%; Score 73.5; DB 16; Length 371;
Best Local Similarity 28.6%; Pred. No. 63;
Matches 24; Conservative 17; Mismatches 32; Indels 11; Gaps 3;
QY 10 GIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDTAT--ELN 66
DB 13 GITVSCS---GNIVTFASFLQDQYNQSCQYQNA-----LKSVDIENKIEALDNIQIGELN 64
QY 67 NALQNLTARTISEAGQAMASTEGNV 90
DB 65 NSINDTKRINESQNWAIQGX 88
RESULT 22
ID Q9ZIX5 PRELIMINARY; PRT; 389 AA.
AC Q9ZIX5;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-MAY-2003 (TREMELrel. 23, Last annotation update)
DE Mip22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AL168;
RA Thern A., Wustfelt M., Lindahl G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

-!- SUBCELLULAR LOCATION: ATTACHED TO THE CELL WALL PEPTIDOGLYCAN BY
AN AMIDE BOND (BY SIMILARITY).
EMBL; AF007557; AAD01409.1; -
DR InterPro; IPR005877; Gpos_YSIK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR InterPro; IPR006192; LPXTG.
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIK signal; 1.
DR PRINTS; PR00015; GPOSANCHOR.
DR TIGRFAMs; TIGR01167; LPXTG anchor; 1.
DR TIGRFAMs; TIGR01168; YSIK signal; 1.
DR PROSITE; PS0847; GRAM_POS_ANCHORING; 1.
KW Cell wall; Peptidoglycan-anchor.
SQ SEQUENCE 389 AA; 42424 MW; 68F2EC0FCF15C5EC CRC64;
Query Match 15.3%; Score 73.5; DB 2; Length 389;
Best Local Similarity 24.4%; Pred. No. 67;
Matches 21; Conservative 19; Mismatches 41; Indels 5; Gaps 1;
QY 1 MTEQQNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
DB 204 LTELQAKLDTATAEKAKLESRTTLENLIGSAKRELTDLQAKLDASNAE-----KEKLOS 258
QY 61 TATELNALQNLTARTISEAGQAMAST 86
DB 259 QAATLEKQLEATKKEKLADLQAKLAAT 284
RESULT 23
ID Q8E2M9 PRELIMINARY; PRT; 772 AA.
AC Q8E2M9;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE Hypothetical protein.
GN GBS2093.
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevallier F., Frangeul L.,
Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
Kunst F.;
RA "Genome sequence of Streptococcus agalactiae, a pathogen causing
invasive neonatal disease";
RL Mol. Microbiol. 45:1499-1513 (2002).
DR EMBL; AL766856; CAD47752.1; -
DR Sagalish; gbs2093; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 772 AA; 82819 MW; 4F3B4A11DE20A850 CRC64;
Query Match 15.3%; Score 73.5; DB 16; Length 772;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
Matches 22; Conservative 12; Mismatches 47; Indels 3; Gaps 2;
QY 10 GIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDTAT--ATELNN 67
DB 238 GLETLSDGVATYTTGVHK-LSEGSQKLDKSAQALVEGSEKLTDLGLQSLQATLKPQER 296
QY 68 ALQNLTARTISEAGQAMASTEGNV 91
DB 297 TLQNLSDGLKNLNLQITNLQSTAT 320
RESULT 24
ID Q8DWS9 PRELIMINARY; PRT; 772 AA.
AC Q8DWS9;

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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Membrane protein, putative.
GN SAG2134.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masiugnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL; AE014288; AAN00992.1; -.
DR TIGR; SAG2134; -.
KW Complete proteome.
SQ SEQUENCE 772 AA; 82807 MW; D4B027A703DCA790 CRC64;

Query Match 15.3%; Score 73.5; DB 16; Length 772;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
Matches 22; Conservative 12; Mismatches 4; Indels 3; Gaps 2;

QY 10 GIEAASAIQGNVTSIHSLLEGKQSLTKLAAAGSGSEAYQGVQKWDAT--ATELNN 67
DB 238 GLETLSDGVTAYTTGVHK-LSEGSQKLDKQALVEGSEKLTGDI-QQLSQATQLKPEQR 296
QY 68 ALQNLARTISEAGAMASTEAGNTV 91
DB 297 TLQNLSDGLKLNLIITNLQSTAT 320

RESULT 25
Q8EZK6 PRELIMINARY; PRT; 2785 AA.
ID Q8EZK6
AC Q8EZK6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Probable phenazine biosynthesis family protein.
GN LA3725.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiroaceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011528; AAN50923.1; -.
KW Complete proteome.
SQ SEQUENCE 2785 AA; 305026 MW; 743BB099DD3C4930 CRC64;

Query Match 15.3%; Score 73.5; DB 16; Length 2785;
Best Local Similarity 25.2%; Pred. No. 7.9e+02;
Matches 31; Conservative 21; Mismatches 32; Indels 39; Gaps 8;

QY 3 EQQNFAGIEAASAIQGNVTSIH-----SLLDEGKQSLTKLAAAGG-----SGS 48
DB 164 QSQWD-----SFVSGNGLNLMNGSLSTVLNSQQTLEGLGQWWDNFQNNLQSG 215
QY 49 EAYQ----GVQKWDATATLNNALQNLARTI-----SEAG---QAMASTEAG-----NVT 91

RESULT 26
Q8F850 PRELIMINARY; PRT; 3141 AA.
ID Q8F850
AC Q8F850;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN LA0709.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiroaceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RA Ren S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE011258; AAN47908.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 3141 AA; 343535 MW; B931EDC3DA2915F CRC64;

Query Match 15.3%; Score 73.5; DB 16; Length 3141;
Best Local Similarity 25.2%; Pred. No. 9.1e+02;
Matches 31; Conservative 21; Mismatches 32; Indels 39; Gaps 8;

QY 3 EQQNFAGIEAASAIQGNVTSIH-----SLLDEGKQSLTKLAAAGG-----SGS 48
DB 166 QSQWD-----SFVSGNGLNLMNGSLSTVLNSQQTLEGLGQWWDNFQNNLQSG 217
QY 49 EAYQ----GVQKWDATATLNNALQNLARTI-----SEAG---QAMASTEAG-----NVT 91
DB 218 QTYQQAAGLTKYQNLINQINQTELQYQAHLAQIQSQAGIKQILSLLEGYQSFLNS 277
QY 92 GMF 94
DB 278 GLF 280

RESULT 27
Q960H0 PRELIMINARY; PRT; 760 AA.
ID Q960H0
AC Q960H0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SD02289p.
GN TOR OR CG5092.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise B., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052068; AAK93492.1; -.
DR FlyBase; FBgn0021796; Tor.
DR InterPro; IPR003151; FATC.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000403; P13_P14_kinase.

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DR Pfam; PF02259; FAT; 1.  
DR Pfam; PF02260; FATC; 1.  
DR Pfam; PF00454; P13_P14_kinase; 1.  
DR SMART; SM00146; PI3KC; 1.  
DR PROSITE; PS00915; P13_4_KINASE_1; 1.  
DR PROSITE; PS00916; P13_4_KINASE_2; 1.  
DR PROSITE; PS02290; P13_4_KINASE_3; 1.  
SQ SEQUENCE 760 AA; 86888 MW; A081D76114080BE0 CRC64;  
  
Query Match 15.2%; Score 73; DB 5; Length 760;  
Best Local Similarity 25.5%; Pred.No.1.7e+02;  
Matches 24; Conservative 22; Mismatches 28; Indels 20; Gaps 5;  
  
QY 4 QQNFAGIEAASAIQGN-----VTSIHSLLDEGKQS--TKLAAWGGSGSEAYQ 52  
   :|::||::||::||::||::||::||::||::||::||::||::||::||:  
Db 236 EQWH-EGLEASRLYFGDRNVKMFEILPEHLAWLERGPQTLLKETSFSAIGRELTEAYE 294  
   ::||::||::||::||::||::||::||::||::||::||::||::||:  
  
QY 53 GVQQ-KWDATATELNNA-----LQNLARTISE 78  
   :|::||::||::||::||::||::||::||::||::||::||::||:  
Db 295 WSQRYKTSAVVMDLDRAWDIYHVFKISRQLPQ 328  
   :|::||::||::||::||::||::||::||::||::||::||::||:  
  
RESULT 28  
Q915S5 PRELIMINARY; PRT; 1204 AA.  
ID AC Q915S5;  
AC AC Q915S5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DB Probable bacteriophage protein.  
GN PA0641.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI_TaxId=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 15692 / PA01;  
RX MEDLINE=2043737; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,  
RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadnan S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an  
RT opportunistic pathogen";  
RL Nature 406:959-964(2000).  
DR EMBL; AE004499; AAG04030.1; --  
DR InterPro; IPRO03961; FN III.  
DR SMART; SMO0060; FN3; 1.  
KW Complete proteome.  
SQ SEQUENCE 1204 AA; 130789 MW; 9090BE6D712F759 CRC64;  
  
Query Match 15.2%; Score 73; DB 16; Length 1204;  
Best Local Similarity 23.7%; Pred.No.3.1e+02;  
Matches 23; Conservative 25; Mismatches 35; Indels 14; Gaps 4;  
  
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   :|::||::||::||::||::||::||::||::||::||::||::||::||:  
Db 993 LEARYADAEGRIATVERVATSDRQAQLDQLSASIGCTTAASIQSEQETARANADSALAQ 1052  
   :|::||::||::||::||::||::||::||::||::||::||::||::||:  
  
QY 65 LNNAIQNLART-----ISEAGQMASTEGNVTGMFA 95  
   :|::||::||::||::||::||::||::||::||::||::||::||:  
Db 1053 RIDTVQ--ARTDTNSAAIQTTTSAVTSLDGNVKAMYS 1087  
   :|::||::||::||::||::||::||::||::||::||::||::||:  
  
RESULT 29  
Q9VK45 PRELIMINARY; PRT; 2470 AA.  
ID AC Q9VK45;  
AC AC Q9VK45;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Search completed: February 5, 2004, 17:40:02
Job time : 17.7976 secs

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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:36:54 ; Search time 6.3333 Seconds
(without alignments)
634.663 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQOWNFAGTEAAASATQG.....ISEAQWASIEGNTGMPA 95

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 306088

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 90 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	479	100.0	95	2	US-08-465-640-2
2	259	54.1	51	3	US-08-818-112-104
3	259	54.1	51	4	US-08-818-111-99
4	259	54.1	51	4	US-09-056-556-104
5	259	54.1	51	4	US-09-072-596-99
6	80	16.7	500	1	US-08-260-582-77
7	80	16.7	500	5	PCT-US95-05471-77
8	75	15.7	504	4	US-09-252-991A-26180
9	73	15.2	1207	4	US-09-252-991A-27470
10	71.5	14.9	94	4	US-09-073-009-21
11	71.5	14.9	94	4	US-09-073-009-31
12	71	14.8	94	4	US-09-073-009-23
13	70.5	14.7	94	4	US-09-073-009-19
14	70.5	14.7	94	4	US-09-073-009-29
15	70.5	14.7	331	4	US-09-223-040-4
16	68.5	14.3	94	4	US-09-073-009-27
17	67.5	14.1	475	4	US-09-252-991A-20838
18	67	14.0	445	4	US-09-477-135A-135
19	67	14.0	2293	3	US-09-368-590-2
20	66.5	13.9	94	4	US-09-073-009-25
21	66	13.8	185	2	US-08-691-814B-12
22	66	13.8	185	4	US-09-250-609-11
23	66	13.8	185	4	US-09-250-611-11
24	66	13.8	548	4	US-08-985-492-15
25	65.5	13.7	465	4	US-09-411-132A-6
26	65.5	13.7	465	4	US-09-411-132A-6
27	65.5	13.7	525	4	US-09-187-999-9

ALIGNMENTS

RESULT 1

US-08-465-640-2
; Sequence 2, Application US/08465640
; Patent No. 5955077
; GENERAL INFORMATION:

28	65.5	13.7	537	4	US-09-252-991A-20929	Sequence 20929, A
29	65	13.6	95	4	US-08-311-731A-79	Sequence 79, Appl
30	65	13.6	112	4	US-08-311-731A-185	Sequence 185, App
31	65	13.6	319	4	US-09-198-452A-893	Sequence 893, App
32	65	13.6	1057	4	US-09-107-532A-4789	Sequence 4789, App
33	65	13.6	1151	4	US-09-328-352-4744	Sequence 4744, Ap
34	64.5	13.5	461	1	US-08-186-222-2	Sequence 2, Appli
35	64.5	13.5	476	2	US-08-955-713-4	Sequence 4, Appli
36	64.5	13.5	530	4	US-09-252-991A-23861	Sequence 23861, A
37	64.5	13.5	1043	4	US-08-851-567B-61	Sequence 61, Appl
38	64	13.4	189	1	US-08-884-682-4	Sequence 4, Appli
39	64	13.4	189	2	US-09-096-082-4	Sequence 4, Appli
40	64	13.4	293	3	US-09-252-991A-27425	Sequence 27425, A
41	64	13.4	562	3	US-09-012-515A-14	Sequence 14, Appl
42	64	13.4	562	3	US-08-360-144A-14	Sequence 14, Appl
43	64	13.4	562	4	US-09-012-504A-14	Sequence 14, Appl
44	64	13.4	562	4	US-09-012-399A-14	Sequence 14, Appl
45	64	13.4	562	4	PCT-US95-06722-14	Sequence 14, Appl
46	64	13.4	1209	4	US-09-252-991A-25844	Sequence 25844, A
47	64	13.4	3031	1	US-07-689-008-2	Sequence 2, Appli
48	63.5	13.3	690	4	US-09-252-991A-23187	Sequence 23187, A
49	63.5	13.3	975	4	US-09-914-259-19	Sequence 19, Appl
50	63.5	13.3	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
51	63	13.2	247	4	US-09-252-991A-29972	Sequence 29972, A
52	63	13.2	272	4	US-09-252-991A-28312	Sequence 28312, A
53	63	13.2	857	4	US-09-252-991A-23956	Sequence 23956, A
54	63	13.2	1477	1	US-08-038-682-4	Sequence 4, Appli
55	63	13.2	1477	2	US-08-302-832-4	Sequence 4, Appli
56	63	13.2	1477	2	US-08-530-198-4	Sequence 4, Appli
57	63	13.2	1477	2	US-08-469-880-4	Sequence 4, Appli
58	63	13.2	1477	2	US-08-728-470-4	Sequence 4, Appli
59	63	13.2	1477	2	US-08-617-697-4	Sequence 4, Appli
60	63	13.2	1477	3	US-08-719-641-4	Sequence 4, Appli
61	62.5	13.0	3729	2	US-08-804-227C-4	Sequence 4, Appli
62	62	12.9	130	4	US-09-732-210-1130	Sequence 1130, Ap
63	62	12.9	278	4	US-09-252-991A-21844	Sequence 21844, A
64	62	12.9	2504	4	US-09-328-352-5821	Sequence 5821, Ap
65	61.5	12.8	190	1	US-08-106-981-2	Sequence 2, Appli
66	61.5	12.8	316	4	US-09-308-375-3	Sequence 3, Appli
67	61.5	12.8	414	4	US-09-252-991A-31151	Sequence 31151, A
68	61.5	12.8	497	4	US-09-328-352-7959	Sequence 7959, Ap
69	61.5	12.8	1098	1	US-07-777-715-7	Sequence 7, Appli
70	61.5	12.8	1098	3	US-08-170-126-2	Sequence 2, Appli
71	61.5	12.8	1098	3	US-08-954-418-2	Sequence 2, Appli
72	61.5	12.8	1129	4	US-09-252-991A-29927	Sequence 2, Appli
73	61.5	12.8	4545	2	US-08-804-227C-14	Sequence 14, Appl
74	61.5	12.8	4550	2	US-08-804-227C-8	Sequence 8, Appli
75	61.5	12.8	4550	2	US-08-804-198-2	Sequence 2, Appli
76	61	12.7	304	3	US-09-105-390-40	Sequence 40, Appl
77	61	12.7	331	3	US-09-105-390-56	Sequence 56, Appl
78	61	12.7	347	4	US-09-252-991A-19006	Sequence 19006, A
79	61	12.7	375	3	US-09-863-743-1	Sequence 1, Appli
80	61	12.7	375	4	US-09-590-540-1	Sequence 1, Appli
81	61	12.7	418	3	US-09-141-000-6	Sequence 6, Appli
82	60.5	12.6	330	3	US-09-267-031-16	Sequence 16, Appl
83	60.5	12.6	338	1	US-08-891-254-1	Sequence 1, Appli
84	60.5	12.6	338	2	US-08-484-358-2	Sequence 2, Appli
85	60.5	12.6	338	2	US-08-819-539-1	Sequence 1, Appli
86	60.5	12.6	338	2	US-09-030-270A-1	Sequence 1, Appli
87	60.5	12.6	338	3	US-09-118-959-2	Sequence 2, Appli
88	60.5	12.6	338	3	US-08-984-207-1	Sequence 1, Appli
89	60.5	12.6	338	3	US-09-013-587-1	Sequence 1, Appli
90	60.5	12.6	338	4	US-09-086-118-21	Sequence 21, Appl

APPLICANT: ANDERSEN, Peter
APPLICANT: ANDERSEN, Ase Bengaard
APPLICANT: HASLOV, Kaare
APPLICANT: SORESEN, Anne Lund
TITLE OF INVENTION: TUBERCULOSIS VACCINE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,640
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,182
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK94/00273
FILING DATE: 01-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSEN-3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-640-2

Query Match 100.0%; Score 479; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 6.3e-47;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
DB 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60

QY 61 TATELNALQNLARTISEAQWASTEGNVTGMFA 95
DB 61 TATELNALQNLARTISEAQWASTEGNVTGMFA 95

RESULT 2
US-08-818-112-104
; Sequence 104, Application US/08818112
; Patent No. 6290969
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-112-104

Query Match 54.1%; Score 259; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAWGGSGSEAY 51
DB 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAWGGSGSEAY 51

RESULT 3
US-08-818-111-99
; Sequence 99, Application US/08818111
; Patent No. 6338852
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Houghton, Raymond
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Twardzik, Daniel R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/818,111
; FILING DATE: 13-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.417C6
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-818-111-99

Query Match 54.1%; Score 259; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTEQOWNFAGIEAAASAIQGNVTSHSLDEGKQSLTKLAAWGGSGSEAY 51

RESULT 4

US-09-056-556-104
Sequence 104, Application US/09056556
Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 104:

SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-056-556-104

Query Match 54.1%; Score 259; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAASAIQGNVTSHSLDEGKQSLTKLAAWGGSGSEAY 51
|||||
Db 1 MTEQOWNFAGIEAAASAIQGNVTSHSLDEGKQSLTKLAAWGGSGSEAY 51

RESULT 5

US-09-072-596-99
Sequence 99, Application US/09072596
Patent No. 6458366

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 99:

SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-072-596-99

Query Match 54.1%; Score 259; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.9e-22;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAAASAIQGNVTSHSLDEGKQSLTKLAAWGGSGSEAY 51
|||||
Db 1 MTEQOWNFAGIEAAASAIQGNVTSHSLDEGKQSLTKLAAWGGSGSEAY 51

RESULT 6

US-08-260-582-77
Sequence 77, Application US/08260582
Patent No. 5635182

GENERAL INFORMATION:

APPLICANT: McCoy, John M.
APPLICANT: Lu, Zhijian
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Fri Feb 6 13:54:43 2004

us-09-805-427a-1.116min.ra1

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/260,582

FILING DATE: 16-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAMS: Melkert, M. C.

REGISTRATION NUMBER: 31,544

REFERENCE/DOCKET NUMBER: GI 5236

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-260-582-77

Query Match 16.7%; Score 80; DB 1; Length 500;

Best Local Similarity 30.4%; Pred. No. 0.64;

Matches 24; Conservative 9; Mismatches 38; Indels 8; Gaps 1;

QY 9 AGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKWDATATELNNA 68

Db 396 AGGEALTAVANGKTTDPLKALDDAIAVSDFKRSLSG-----AVQNRLDASVTNLNNT 447

QY 69 LQNLARTISEAGQAMASTE 87

Db 448 TTNLSEAQSRIQADYATE 466

RESULT 7

PCT-US95-05471-77

Sequence 77, Application PC/TUS9505471

GENERAL INFORMATION:

APPLICANT: METHOD OF DETECTING LIGAND INTERACTIONS

TITLE OF INVENTION: 76

NUMBER OF SEQUENCES: 76

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05471

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 500 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-05471-77

Query Match 16.7%; Score 80; DB 5; Length 500;

Best Local Similarity 30.4%; Pred. No. 0.64;

Matches 24; Conservative 9; Mismatches 38; Indels 8; Gaps 1;

QY 9 AGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKWDATATELNNA 68

Db 396 AGGEALTAVANGKTTDPLKALDDAIAVSDFKRSLSG-----AVQNRLDASVTNLNNT 447

QY 69 LQNLARTISEAGQAMASTE 87

Db 448 TTNLSEAQSRIQADYATE 466

RESULT 8

US-09-252-991A-26180

Sequence 26180, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26180

LENGTH: 504

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26180

Query Match 15.7%; Score 75; DB 4; Length 504;

Best Local Similarity 29.1%; Pred. No. 2.4;

Matches 23; Conservative 12; Mismatches 36; Indels 8; Gaps 2;

QY 8 FAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGGSGSEAYQGVQKWDATATELNN 67

Db 215 FNAMOGYQRIYGVVAAATKLDGAQAARSM---GQVRGMLGQSQETDTATATIN- 269

QY 68 ALQNLARTISEAGQAMASTE 86

Db 270 ---EMSTTVFHLAQHAADT 285

RESULT 9

US-09-252-991A-27470

Sequence 27470, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27470

LENGTH: 1207

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-27470

Query Match 15.2%; Score 73; DB 4; Length 1207;

Best Local Similarity 22.8%; Pred. No. 13;

Matches 23; Conservative 23; Mismatches 33; Indels 22; Gaps 4;

QY 11 IEAASAIQGNVTSHSLDEGKQS-----ITKLAAAWGGSG-----SEAYQGVQ 56

Db 996 LEARTADAGRIATVSRVATSDQATQRLDQLSASIGTAAASLQSEQTARANADSALAQ 1055

QY 57 KWDA--TATLNNALQNLARTISEAGQAMASTEAGVTGMEFA 95

Db 1056 RIDTVQASTDTNSA-----AIQTTTQAVTSLDGNVKMYS 1090

RESULT 10

US-09-073-009-21

Sequence 21, Application US/09073009

Patent No. 6555653

GENERAL INFORMATION:

APPLICANT: Alderson, Mark

APPLICANT: Dillon, Davin C.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Cumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: single
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-21

Query Match 14.9%; Score 71.5; DB 4; Length 94;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;
QY 6 WNFAGIEAASAIQGNVTSHSLDEGKQSLTK--LAAA--WGGSGSEAYQG----- 53
Db 5 YQGDVDHAGMIRAQA---GLLEABHQAIIRDVLTA SDFWGGAGSAA CCGFTITQLGRN 60
QY 54 ---VQKWDATATLNNALQNLARTISEAGQAMA 84
Db 61 FQVIVEQANAHGQKVQAGNNAQTDSAVGSSWA 94

RESULT 11
US-09-073-009-31
Sequence 31, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Cumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-31

Query Match 14.9%; Score 71.5; DB 4; Length 94;
Best Local Similarity 25.5%; Pred. No. 0.64;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;
QY 6 WNFAGIEAASAIQGNVTSHSLDEGKQSLTK--LAAA--WGGSGSEAYQG----- 53
Db 5 YQGDVDHAGMIRAQA---GLLEABHQAIIRDVLTA SDFWGGAGSAA CCGFTITQLGRN 60
QY 54 ---VQKWDATATLNNALQNLARTISEAGQAMA 84
Db 61 FQVIVEQANAHGQKVQAGNNAQTDSAVGSSWA 94

RESULT 12
US-09-073-009-23
Sequence 23, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Cumbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid

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us-09-805-427a-1.116min.ra1

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
;
US-09-073-009-23
Query Match 14.8%; Score 71; DB 4; Length 94;
Best Local Similarity 25.7%; Pred. No. 0.73;
Matches 26; Conservative 17; Mismatches 36; Indels 22; Gaps 5;

Qy 6 WNFAGIEAASAIQGNVTSHSLDEGKQSLTK--LAAA--WGGSGSEAYQGVQKWDAT 61
Db 5 YQFGVDVDAHGMIRAQ--GLAEHQAIKIRVLTASDFWGGAGSAACQGF----- 53
Qy 62 ATELNALQNL-----ARTISEAGQAMASTEAGNVTCMFA 95
Db 54 ITQLGRNFQVIEQANTHGKQVQAAGNNMAQTDSAVXSSWA 94

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RESULT 13
US-09-073-009-19
; Sequence 19, Application US/09073009
; Patent No. 6555653
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,009
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.441C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
;
US-09-073-009-19
Query Match 14.7%; Score 70.5; DB 4; Length 94;
Best Local Similarity 25.5%; Pred. No. 0.83;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

Qy 6 WNFAGIEAASAIQGNVTSHSLDEGKQSLTK--LAAA--WGGSGSEA----- 50
Db 5 YQFGVDVDAHGMIRAAQAS---LEAEHQAIKIRVLDVLAAGDFWGGAGSVACQEFITQLGRN 60

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Qy 51 YQGVQKWDATATELNNALONLARTISEAGQAMA 84
Db 61 FQVIYEQANAHGKQVQAAGNNMAQTDSAVGSSWA 94

RESULT 14
US-09-073-009-29
; Sequence 29, Application US/09073009
; Patent No. 6555653
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, David C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,009
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.441C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
;
US-09-073-009-29
Query Match 14.7%; Score 70.5; DB 4; Length 94;
Best Local Similarity 25.5%; Pred. No. 0.83;
Matches 24; Conservative 21; Mismatches 30; Indels 19; Gaps 4;

Qy 6 WNFAGIEAASAIQGNVTSHSLDEGKQSLTK--LAAA--WGGSGSEAYQG----- 53
Db 5 YQFGVDVDAHGMIR---ALAGLEAEHQAIISDVLTASDFWGGAGSAACQGFITQLGRN 60
Qy 54 ---VQKWDATATELNNALONLARTISEAGQAMA 84
Db 61 FQVIYEQANAHGKQVQAAGNNMAQTDSAVGSSWA 94

```

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RESULT 15
US-09-223-040-4
; Sequence 4, Application US/09223040
; Patent No. 6544522
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Alderson, Mark
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens
;

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;; TITLE OF INVENTION: and Their Uses
;; FILE REFERENCE: 014058-009010US
;; CURRENT APPLICATION NUMBER: US/09/223,040
;; CURRENT FILING DATE: 1998-12-30
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 331
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: tri-fusion
US-09-223-040-4

Query Match 14.7%; Score 70.5; DB 4; Length 331;
Best Local Similarity 25.5%; Pred. No. 4.4;
Matches 24; Conservative 20; Mismatches 31; Indels 19; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKQSLTK--LAAA--WGGSGSEA-----50
Db 242 YQFGVDVDAHGMIRAAAS----LEAEHQAIYRDVLAAGDFWGGAGSVACQEFITQLGRN 297
QY 51 YQGVQCKWDATATLNNALQNLARTISEAQMA 84
Db 298 FQVIEQANAHGQKVQAAGNNNAQTDSAVGSSWA 331

RESULT 16
US-09-073-009-27
; Sequence 27, Application US/09073009
; Patent No. 6555653
; GENERAL INFORMATION:
; APPLICANT: Alderson, Mark
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Campos-Neto, Antonio
; TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Cumbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-MAY-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.441C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-09-073-009-27

Query Match 14.3%; Score 68.5; DB 4; Length 94;

Best Local Similarity 25.5%; Pred. No. 1.4;
Matches 24; Conservative 19; Mismatches 32; Indels 19; Gaps 4;
QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKQSLTK--LAAA--WGGSGSEAYQG-----53
Db 5 YQFGVDVDAHGMIRAXA---GLLEAEHQAIISDVLTSDFWGGAGSAACQGFITQLGRN 60
QY 54 ---VQCKWDATATLNNALQNLARTISEAQMA 84
Db 61 FQVIEQANAHGQKVQAAGNNNAQTDSAVGSSWA 94

RESULT 17
US-09-252-991A-20838
; Sequence 20838, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20838
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20838

Query Match 14.1%; Score 67.5; DB 4; Length 475;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 24; Conservative 17; Mismatches 38; Indels 11; Gaps 4;

QY 6 WNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGGSGSEAYQGVQCKWDATATL 65
Db 267 WHPAGVEAGGEGVGNGPRG-----DFAHPSQRRQAGA-GGPGAEQRRQRRAHQGPQDL 320
QY 66 NNALQN--LARTISEAQMASTEAGNVGTGM 93
Db 321 AHALQEVLMVDVEDHGESRRSV---VAGL 347

RESULT 18
US-09-477-135A-135
; Sequence 135, Application US/09477135A
; Patent No. 6572865
; GENERAL INFORMATION:
; APPLICANT: Nano, Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; TITLE OF INVENTION: Immunostimulatory Peptides
; FILE REFERENCE: 52888
; CURRENT APPLICATION NUMBER: US/09/477,135A
; CURRENT FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 08990823
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 96/10375
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: 60/000,254
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 135
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-135

Query Match 14.0%; Score 67; DB 4; Length 445;

Best Local Similarity 25.9%; Pred. No. 16;
Matches 22; Conservative 14; Mismatches 33; Indels 16; Gaps 2;

QY 9 AGTAAASAIQGNVTSHSLDEGKSLTKLAAAGGSGSEAYQGVQKWDATATLNNNA 68
DB 159 AAINQAADTLDGNGDSLHNLRE---LAQVAGRLGDSRGDIFGTGKN----- 202

QY 69 LONLARTISEAGQAMATEGNTVM 93
DB 203 LQVLVDALSESDEQIVQFAGHVASV 227

RESULT 19
US-09-368-590-2
Sequence 2, Application US/09368590
Patent No. 6187563
GENERAL INFORMATION:
APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2293
TYPE: PRT
ORGANISM: Human
US-09-368-590-2

Query Match 14.0%; Score 67; DB 3; Length 2293;
Best Local Similarity 26.2%; Pred. No. 1.4e+02;
Matches 21; Conservative 16; Mismatches 29; Indels 14; Gaps 4;

QY 5 QWNFAGIEAASAIQGNVTSHSLDEGKSLTKLAAAGGSGSEAYQGVQ---KWDAT 61
DB 719 QWFLSGLERAIQALEPRQA---ALLEEA---ALLAERFPQAAXLHOGAEIIGAEMGAL 771

QY 62 ATELNALQNLARTISEAGQ 81
DB 772 A-----SAAQACGEAVAAAGR 787

RESULT 20
US-09-073-009-25
Sequence 25, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-25

Query Match 13.9%; Score 66.5; DB 4; Length 94;
Best Local Similarity 23.7%; Pred. No. 2.3;
Matches 22; Conservative 20; Mismatches 34; Indels 17; Gaps 3;

QY 6 WNFAGIEAASAIQGNVTSHSLDEGKSLTKLAAA---WGGSGSEAYQG----- 53
DB 5 YQFGVDVDAHGAMIRAQAGSLEA---EHOAISDLVLTASDFWGGAGSAAACQGFITQLGRNF 61

QY 54 --VQOKWDATATLNNALQNLARTISEAGQAMA 84
DB 62 QVXYEQANAHGKQVQAAGNNNAQTDSAVGSSWA 94

RESULT 21
US-08-691-814B-12
Sequence 12, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Bassett, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid

Best Local Similarity 25.9%; Pred. No. 16;
Matches 22; Conservative 14; Mismatches 33; Indels 16; Gaps 2;

QY 9 AGTAAASAIQGNVTSHSLDEGKSLTKLAAAGGSGSEAYQGVQKWDATATLNNNA 68
DB 159 AAINQAADTLDGNGDSLHNLRE---LAQVAGRLGDSRGDIFGTGKN----- 202

QY 69 LONLARTISEAGQAMATEGNTVM 93
DB 203 LQVLVDALSESDEQIVQFAGHVASV 227

RESULT 19
US-09-368-590-2
Sequence 2, Application US/09368590
Patent No. 6187563
GENERAL INFORMATION:
APPLICANT: Solimena, Michele
TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2293
TYPE: PRT
ORGANISM: Human
US-09-368-590-2

Query Match 14.0%; Score 67; DB 3; Length 2293;
Best Local Similarity 26.2%; Pred. No. 1.4e+02;
Matches 21; Conservative 16; Mismatches 29; Indels 14; Gaps 4;

QY 5 QWNFAGIEAASAIQGNVTSHSLDEGKSLTKLAAAGGSGSEAYQGVQ---KWDAT 61
DB 719 QWFLSGLERAIQALEPRQA---ALLEEA---ALLAERFPQAAXLHOGAEIIGAEMGAL 771

QY 62 ATELNALQNLARTISEAGQ 81
DB 772 A-----SAAQACGEAVAAAGR 787

RESULT 20
US-09-073-009-25
Sequence 25, Application US/09073009
Patent No. 6555653
GENERAL INFORMATION:
APPLICANT: Alderson, Mark
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: COMPOUNDS AND DIAGNOSIS OF
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Ave.
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,009
FILING DATE: 05-MAY-1998
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.441C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
US-09-073-009-25

Query Match 13.9%; Score 66.5; DB 4; Length 94;
Best Local Similarity 23.7%; Pred. No. 2.3;
Matches 22; Conservative 20; Mismatches 34; Indels 17; Gaps 3;

QY 6 WNFAGIEAASAIQGNVTSHSLDEGKSLTKLAAA---WGGSGSEAYQG----- 53
DB 5 YQFGVDVDAHGAMIRAQAGSLEA---EHOAISDLVLTASDFWGGAGSAAACQGFITQLGRNF 61

QY 54 --VQOKWDATATLNNALQNLARTISEAGQAMA 84
DB 62 QVXYEQANAHGKQVQAAGNNNAQTDSAVGSSWA 94

RESULT 21
US-08-691-814B-12
Sequence 12, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Bassett, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383.0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid

TUBERCULOSIS AND ME

ATTORNEY/AGENT INFORMATION:
 NAME: Fehner Ph.D., Paul F.
 REGISTRATION NUMBER: 35,135
 REFERENCE/DOCKET NUMBER: A2582-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610)454-3839
 TELEFAX: (610)454-3808
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 465 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-985-492-15

Query Match 13.7%; Score 65.5; DB 4; Length 465;
 Best Local Similarity 19.5%; Pred. No. 25;
 Matches 25; Conservative 16; Mismatches 46; Indels 41; Gaps 3;
 QY 7 NFAGIEAASAIQGNVTS-----IHSLLDEGK-----QSLTKLAANG 44
 Db 65 NFQEAADSSISGSGNFKNRKTFRILHGFIDKGEENLANVCKNLFKVESVNCICVDWK 124
 QY 45 GSGSEAYQGVQKWDATATLNNALQNL-----ARTISEAQAMAS 85
 Db 125 GGSRTGYTQASQNIIRIVGAEVYFVEFLQSAFGYSPSNVHVHIGSLGHAAGEAGRTNG 184
 QY 86 TEGNVGM 93
 Db 185 TIGRTGL 192

RESULT 26

US-09-411-132A-6
 Sequence 6, Application US/09411132A
 Patent No. 6558936
 GENERAL INFORMATION:
 APPLICANT: Rhodadoust, Mehran
 APPLICANT: Kapeller-Libermann, Rosana
 TITLE OF INVENTION: No. 6558936el Human Lipase Proteins, Nucleic Acides Encoding
 TITLE OF INVENTION: Them, and Uses of Both of These
 FILE REFERENCE: 10147-14
 CURRENT APPLICATION NUMBER: US/09/411,132A
 PRIOR FILING DATE: 2000-09-12
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 465
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-411-132A-6

Query Match 13.7%; Score 65.5; DB 4; Length 465;
 Best Local Similarity 19.5%; Pred. No. 25;
 Matches 25; Conservative 16; Mismatches 46; Indels 41; Gaps 3;
 QY 7 NFAGIEAASAIQGNVTS-----IHSLLDEGK-----QSLTKLAANG 44
 Db 65 NFQEAADSSISGSGNFKNRKTFRILHGFIDKGEENLANVCKNLFKVESVNCICVDWK 124
 QY 45 GSGSEAYQGVQKWDATATLNNALQNL-----ARTISEAQAMAS 85
 Db 125 GGSRTGYTQASQNIIRIVGAEVYFVEFLQSAFGYSPSNVHVHIGSLGHAAGEAGRTNG 184
 QY 86 TEGNVGM 93
 Db 185 TIGRTGL 192

RESULT 27

US-09-187-999-9
 Sequence 9, Application US/09187999A

Patent No. 6482646
 GENERAL INFORMATION:
 APPLICANT: Gindullis, Frank
 APPLICANT: Meier, Iris
 TITLE OF INVENTION: Plant Proteins that Interact with Nuclear Matrix
 TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
 FILE REFERENCE: CL-1321
 CURRENT APPLICATION NUMBER: US/09/187,999A
 CURRENT FILING DATE: 1998-11-06
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 9
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Lycopersicon esculentum
 US-09-187-999-9

Query Match 13.7%; Score 65.5; DB 4; Length 525;
 Best Local Similarity 29.1%; Pred. No. 29;
 Matches 34; Conservative 13; Mismatches 41; Indels 29; Gaps 6;
 QY 1 MTEQQWNT-AGTEAASAIQ-----GNVTSI-HSLLEDEG-----KQSLTKLAA 41
 Db 275 LTESIFNTHRAAGEALLASIQKEIGKDTNFGHSLVDGIPSNFTSDSDDFRSSTSVL- 333
 QY 42 AWGSGSGSEAYQGVQKWDATATLNNALQN-----LARTISEAQAMASTEAGVTGMEA 95
 Db 334 -----SQNRDGAQSSLSNSEVYSLKQNIILLQNVQEAADLAKSEARVTELEA 384

RESULT 28

US-09-252-991A-20929
 Sequence 20929, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 20929
 LENGTH: 537
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20929

Query Match 13.7%; Score 65.5; DB 4; Length 537;
 Best Local Similarity 21.7%; Pred. No. 30;
 Matches 20; Conservative 16; Mismatches 47; Indels 9; Gaps 1;
 QY 11 IEAASAIQGNVTSIHSLLDEGKQSLTKLAAANGSGSEAYQGVQ-----KWDAT 61
 Db 409 VRSLNPTQOSTQEIQGLIEQLQDGDANDAVAAWRGSSASHAQSNLVEADSAALGRIVAT 468
 QY 62 ATELNNALQNARTISEAQAMASTEAGVTGM 93
 Db 469 VEELDGLNQIATAAEQSQVAQDIDRNTINV 500

RESULT 29

US-08-311-731A-79
 Sequence 79, Application US/08311731A
 Patent No. 6583266
 GENERAL INFORMATION:
 APPLICANT: SMITH, DOUGLAS
 APPLICANT: MAO, JEN-I
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RESULT 30
US-08-311-731A-185
; Sequence 185, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

Search completed: February 5, 2004, 17:41:21
Job time : 7.33333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 5, 2004, 17:38:58 : Search time 13.119 Seconds
(without alignments)
1516.217 Million cell updates/sec

Title: US-09-805-427A-1
Perfect score: 479
Sequence: 1 MTEQWNFAGIEAASAIQ.....ISERAGMASTEGNVTGMFA 95

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 788294

Minimum DB seq length: 6
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap:*
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6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap:*
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	479	100.0	95 10	US-09-805-427A-1	Sequence 1, Appli
2	479	100.0	95 12	US-09-872-505-1	Sequence 1, Appli
3	479	100.0	403 9	US-09-791-171-173	Sequence 173, Appli
4	479	100.0	403 10	US-09-805-427A-4	Sequence 4, Appli
5	479	100.0	403 12	US-09-804-980-173	Sequence 173, Appli
6	479	100.0	403 12	US-09-872-505-4	Sequence 4, Appli
7	479	100.0	404 9	US-09-791-171-172	Sequence 172, Appli
8	479	100.0	404 10	US-09-805-427A-3	Sequence 3, Appli
9	479	100.0	404 12	US-09-804-980-172	Sequence 172, Appli
10	479	100.0	404 12	US-09-872-505-3	Sequence 3, Appli
11	259	54.1	51 12	US-10-084-843-104	Sequence 104, Appli
12	259	54.1	51 12	US-10-193-002-99	Sequence 99, Appli
13	259	54.1	51 12	US-10-098-732A-33	Sequence 33, Appli
14	186	38.8	95 16	US-10-080-170-11	Sequence 11, Appli
15	151	31.5	96 10	US-09-738-626-4145	Sequence 4145, Ap

16	101	21.1	20	10	US-09-813-333-60	Sequence 60, Appli
17	101	21.1	20	14	US-10-044-703-60	Sequence 60, Appli
18	98	20.5	20	10	US-09-813-333-62	Sequence 62, Appli
19	98	20.5	20	14	US-10-044-703-62	Sequence 62, Appli
20	97	20.3	20	10	US-09-813-333-61	Sequence 61, Appli
21	97	20.3	20	14	US-10-044-703-61	Sequence 61, Appli
22	96	20.0	96	12	US-09-804-980-175	Sequence 175, Appli
23	96	20.0	96	12	US-09-804-980-199	Sequence 199, Appli
24	89	18.6	99	15	US-10-156-761-10069	Sequence 10069, A
25	85	17.7	96	9	US-09-791-171-2	Sequence 2, Appli
26	85	17.7	96	12	US-09-804-980-2	Sequence 2, Appli
27	85	17.7	96	12	US-09-804-980-195	Sequence 195, Appli
28	85	17.7	96	16	US-10-080-170-378	Sequence 378, Appli
29	81.5	17.0	108	10	US-09-738-626-4144	Sequence 4144, Ap
30	81	16.9	15	10	US-09-916-201-7	Sequence 7, Appli
31	81	16.9	96	16	US-10-080-170-299	Sequence 299, Appli
32	79	16.5	15	12	US-10-079-167-79	Sequence 79, Appli
33	79	16.5	15	12	US-10-345-000-1	Sequence 1, Appli
34	78.5	16.4	368	9	US-09-287-849-24	Sequence 24, Appli
35	78.5	16.4	368	12	US-10-359-460-24	Sequence 24, Appli
36	78.5	16.4	600	9	US-09-387-849-22	Sequence 22, Appli
37	78.5	16.4	600	12	US-10-359-460-22	Sequence 22, Appli
38	77	16.1	15	12	US-10-079-167-80	Sequence 80, Appli
39	77	16.1	15	12	US-10-345-000-2	Sequence 2, Appli
40	76.5	16.0	837	9	US-09-815-242-5883	Sequence 5883, Ap
41	76.5	16.0	875	9	US-09-815-242-13080	Sequence 13080, A
42	76.5	16.0	2434	9	US-09-815-242-5835	Sequence 5835, Ap
43	76.5	16.0	6281	9	US-09-815-242-12996	Sequence 12996, A
44	76	15.9	16	10	US-09-813-333-63	Sequence 63, Appli
45	76	15.9	16	14	US-10-044-703-63	Sequence 63, Appli
46	74.5	15.6	364	10	US-09-756-983-22	Sequence 22, Appli
47	74	15.4	644	12	US-10-369-493-11283	Sequence 11283, A
48	73	15.2	2086	9	US-09-815-242-5629	Sequence 5629, Ap
49	73	15.2	5795	9	US-09-815-242-12610	Sequence 12610, A
50	72.5	15.1	239	9	US-09-287-849-19	Sequence 19, Appli
51	72.5	15.1	239	12	US-10-359-460-19	Sequence 19, Appli
52	72.5	15.1	239	12	US-10-098-732A-47	Sequence 47, Appli
53	72.5	15.1	433	12	US-09-287-849-14	Sequence 14, Appli
54	72.5	15.1	433	12	US-10-359-460-14	Sequence 14, Appli
55	72.5	15.1	710	9	US-09-287-849-16	Sequence 16, Appli
56	72.5	15.1	710	12	US-10-359-460-16	Sequence 16, Appli
57	72.5	15.1	710	12	US-10-098-732A-49	Sequence 49, Appli
58	72.5	15.1	856	9	US-09-287-849-12	Sequence 12, Appli
59	72.5	15.1	856	12	US-10-359-460-12	Sequence 12, Appli
60	72	15.0	15	10	US-09-916-201-5	Sequence 5, Appli
61	72	15.0	573	15	US-10-043-487-327	Sequence 327, Ap
62	72	15.0	685	12	US-10-158-034-96	Sequence 96, Appli
63	72	15.0	1225	12	US-10-158-034-76	Sequence 76, Appli
64	71.5	14.9	66	9	US-09-864-761-33985	Sequence 33985, A
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66	71.5	14.9	94	9	US-09-073-009-31	Sequence 31, Appli
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69	71.5	14.9	94	9	US-09-793-306-21	Sequence 21, Appli
70	71.5	14.9	94	9	US-09-793-306-31	Sequence 31, Appli
71	71	14.8	94	9	US-09-073-009-23	Sequence 23, Appli
72	71	14.8	94	9	US-09-023-588-23	Sequence 23, Appli
73	71	14.8	94	9	US-09-793-306-23	Sequence 23, Appli
74	70.5	14.7	94	9	US-09-073-009-19	Sequence 19, Appli
75	70.5	14.7	94	9	US-09-073-009-29	Sequence 29, Appli
76	70.5	14.7	94	9	US-09-023-588-19	Sequence 19, Appli
77	70.5	14.7	94	9	US-09-023-588-29	Sequence 29, Appli
78	70.5	14.7	94	9	US-09-793-306-19	Sequence 19, Appli
79	70.5	14.7	94	9	US-09-793-306-29	Sequence 29, Appli
80	70.5	14.7	94	12	US-10-098-732A-27	Sequence 27, Appli
81	70.5	14.7	94	16	US-10-080-170-611	Sequence 611, Appli
82	70.5	14.7	331	12	US-09-287-849-4	Sequence 4, Appli
83	70.5	14.7	331	12	US-10-359-460-4	Sequence 4, Appli
84	70.5	14.7	331	12	US-10-359-459-4	Sequence 4, Appli
85	70.5	14.7	825	12	US-10-369-983-14	Sequence 14, Appli
86	70	14.6	265	10	US-09-738-626-5873	Sequence 5873, Ap
87	69.5	14.5	1029	9	US-09-815-242-5885	Sequence 5885, Ap
88	69.5	14.5	1048	9	US-09-815-242-13083	Sequence 13083, A

89 69 14.4 15 10 US-09-916-201-6 Sequence 6, Appli

90 69 14.4 221 10 US-09-738-626-6507 Sequence 6507, Ap

ALIGNMENTS

RESULT 1

US-09-805-427A-1

; Sequence 1, Application US/09805427A

; Patent No. US20020176867A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut

; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens

; FILE REFERENCE: 670001-2002.5

; CURRENT APPLICATION NUMBER: US/09/805,427A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-09-805-427A-1

Query Match 100.0%; Score 479; DB 10; Length 95;

Best Local Similarity 100.0%; Pred. No. 9.2e-45;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Db 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Qy 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

Db 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 2

US-09-872-505-1

; Sequence 1, Application US/09872505

; Publication No. US20040013685A1

; GENERAL INFORMATION:

; APPLICANT: Statens Serum Institut

; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis

; FILE REFERENCE: 670001-2002.6

; CURRENT APPLICATION NUMBER: US/09/872,505

; CURRENT FILING DATE: 2001-06-01

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Mycobacterium tuberculosis

US-09-872-505-1

Query Match 100.0%; Score 479; DB 12; Length 95;

Best Local Similarity 100.0%; Pred. No. 9.2e-45;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Db 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Qy 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

Db 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

RESULT 3

US-09-791-171-173

; Sequence 173, Application US/09791171

; Patent No. US20020094336A1

GENERAL INFORMATION:

APPLICANT: ANDERSEN, Peter

APPLICANT: NIELSEN, Rikke

APPLICANT: OETTINGER, Thomas

APPLICANT: RASMUSSEN, Peter Birk

APPLICANT: ROSENKRANDS, Ida

APPLICANT: WELDINGH, Karin

APPLICANT: FLORIO, Walter

TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS

TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1

CURRENT APPLICATION NUMBER: US/09/791,171

CURRENT FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: 09/050,739

PRIOR FILING DATE: 1998-03-30

PRIOR APPLICATION NUMBER: 0376/97

PRIOR FILING DATE: 1997-04-02

PRIOR APPLICATION NUMBER: 1277/97

PRIOR FILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/044,624

PRIOR FILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: 60/070,488

PRIOR FILING DATE: 1998-01-05

NUMBER OF SEQ ID NOS: 173

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 173

LENGTH: 403

TYPE: PRT

ORGANISM: Mycobacterium tuberculosis

US-09-791-171-173

Query Match 100.0%; Score 479; DB 9; Length 403;

Best Local Similarity 100.0%; Pred. No. 5.6e-44;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Db 22 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 81

Qy 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

Db 82 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 116

RESULT 4

US-09-805-427A-4

; Sequence 4, Application US/09805427A

; Patent No. US20020176867A1

; GENERAL INFORMATION:

APPLICANT: Statens Serum Institut

TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens

FILE REFERENCE: 670001-2002.5

CURRENT APPLICATION NUMBER: US/09/805,427A

CURRENT FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 403

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B

US-09-805-427A-4

Query Match 100.0%; Score 479; DB 10; Length 403;

Best Local Similarity 100.0%; Pred. No. 5.6e-44;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 60

Db 22 MTEQOWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGSGSEAYQGVQOKWDA 81

Qy 61 TATELNNALQNLARTISEAGQAMASTEAGNVTGMFA 95

```

Db      82 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 116
|||||
RESULT 5
US-09-804-980-173
; Sequence 173, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Andersen, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 173
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-173

Query Match      100.0%; Score 479; DB 12; Length 403;
Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
Db      22 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 81
QY      61 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 95
Db      82 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 116

RESULT 6
US-09-872-505-4
; Sequence 4, Application US/09872505
; Publication No. US20040013685A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872,505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein ESAT-6-Ag85B
US-09-872-505-4

Query Match      100.0%; Score 479; DB 12; Length 403;
Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
Db      22 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 81
QY      61 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 95
Db      82 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 116

RESULT 7
US-09-791-171-172
; Sequence 172, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDLING, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-172

Query Match      100.0%; Score 479; DB 9; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
Db      310 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 369
QY      61 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 95
Db      370 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 404

RESULT 8
US-09-805-427A-3
; Sequence 3, Application US/09805427A
; Patent No. US20020176867A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Hybrids of M. tuberculosis Antigens
; FILE REFERENCE: 670001-2002.5
; CURRENT APPLICATION NUMBER: US/09/805,427A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-805-427A-3

Query Match      100.0%; Score 479; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.6e-44;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 60
Db      310 MTEQQWNFAGIEAAASAIQGNVTSIHSLDDEGKQSLTKLAAAWGGSGSEAYQGVQKQWDA 369
QY      61 TATELNALQNLARTISEAGQAMASTEGNVTGMFA 95

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Fri Feb 6 13:54:44 2004

us-09-805-427a-1.116min.rapb

370 TATELNALQNLARTISEAGQAMASTEGMTGMEA 404

```

RESULT 9
US-09-804-980-172
; Sequence 172, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 172
; LENGTH: 404
; TYPE: PRP
; ORGANISM: Mycobacterium tuberculosis
; US-09-804-980-172

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Query Match	100.0%;	Score 479;	DB 12;	Length 404;
Best Local Similarity	100.0%;	Pred. No. 5.6e-44;		
Matches	95;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY 1 MTEQQNFFAGTEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAAGSGSGSEAYQGVQKWD 60
369 MTEQQNFFAGTEAAASAIQGNVTSIHSLLDEGKQSLTKLAAAAGSGSGSEAYQGVQKWD 369

Qy	61 TATELNALONLARTISEAQOAMASTE GNTGMFA 95
Db	370 TATELNALONLARTISEAQOAMASTE GNTGMFA 404

```

RESULT 10
US-09-872-505-3
; Sequence 3, Application US/09872505
; Publication NO. US20040013685A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; TITLE OF INVENTION: Nucleic Acid Fragments Derived From M. Tuberculosis
; FILE REFERENCE: 670001-2002.6
; CURRENT APPLICATION NUMBER: US/09/872,505
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Fusion protein Ag85B-ESAT-6
US-09-872-505-3

```

Query Match	100.0%;	Score 479;	DB 12;	Length 404;
Best Local Similarity	100.0%;	Pred. No. 5.6e-44;		
Matches	95;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 MTEQQNWFAGIEAAASATQGNVTSIHSLIDEGKQSLTKLAAAGSGSEAYQGVQOKWDA 60

QY	61	TATELNALONLARTISEACQAMASPEGNTGMFA	95
Db	370	TATELNALONLARTISEACQAMASPEGNTGMFA	404

RESULT 11
US-10-084-843-104
; Sequence 104, Application US/10084843
. Publication No. US20030143243A1

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
PS-10--084--843-104

QY 1 MTEQWNFAGIEAAASAIQGNVTSIHSLLDEKQSLTKLAAAWGGSGSEAY 51

RESULT 12
US-10-193-002-99
; Sequence 99, Application US/10193002
; Publication No. US20030135026A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.

Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS

NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-193-002-99

Query Match 54.1%; Score 259; DB 12; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.2e-21;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQOWNFAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGSGSEAY 51
|||||
DB 1 MTEQOWNFAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGSGSEAY 51

RESULT 13
US-10-098-732A-33
; Sequence 33, Application US/10098732A
; Publication No. US20030175294A1
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir
; APPLICANT: Brannon, Mark
; APPLICANT: Guderian, Jeffrey
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Heterologous Fusion Protein Constructs Comprising a
; TITLE OF INVENTION: Leishmania Antigen
; FILE REFERENCE: 014058-012010US
; CURRENT APPLICATION NUMBER: US/10/098,732A
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/275,837
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: ESAT-6
US-10-098-732A-33

Query Match 54.1%; Score 259; DB 12; Length 51;
Best Local Similarity 100.0%; Pred. No. 4.2e-21;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQOWNFAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGSGSEAY 51
|||||
DB 1 MTEQOWNFAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGSGSEAY 51

RESULT 14
US-10-080-170-11
; Sequence 11, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-11

Query Match 38.8%; Score 186; DB 16; Length 95;
Best Local Similarity 36.3%; Pred. No. 8.4e-13;
Matches 33; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

QY 4 QOWNFAGIEAASAIQGNVTSHSLDEGKQSLTKLAAAWGSGSEAYQGVQKWDATAT 63
|||||
DB 3 QAWHFPALQAGVNELOQSQRIDALLEQCQBSLTKLQSSWHGSGNESYSSVQRNFQNTTE 62
|||||
QY 64 ELNNALQNLARTISEAGQAMASTEIGNVTGMF 94
|||||
DB 63 GINHALGDLVQAINHSAETMQOTEAGVNSMF 93

RESULT 15
US-09-738-626-4145
; Sequence 4145, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4145
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum

us-09-805-427a-1.116min.rapb

Fri Feb 6 13:54:44 2004

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US-09-738-626-4145
Query Match      31.5%; Score 151; DB 10; Length 96;
Best Local Similarity 37.5%; Pred. No. 5.6e-09;
Matches 30; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAANGSGSEAYGVQVKWDATATE 64
Db 5 RYEFCAIQGAATDINSTGRINSLDGLKSLQPMVASWEGESSEAYSEAQIKWDRAAAE 64

Qy 65 LNNALQNLARTISEAGQAWA 84
Db 65 LNTILATISNTVAQGAERMS 84

RESULT 16
US-09-813-333-60
; Sequence 60, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-62
Query Match      20.5%; Score 98; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 IQGNVTSIHSLDEGKQSLT 37
Db 1 IQGNVTSIHSLDEGKQSLT 20

RESULT 19
US-10-044-703-62
; Sequence 62, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-62
Query Match      20.5%; Score 98; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 IQGNVTSIHSLDEGKQSLT 37
Db 1 IQGNVTSIHSLDEGKQSLT 20

RESULT 20
US-09-813-333-61
; Sequence 61, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61

US-09-738-626-4145
Query Match      31.5%; Score 151; DB 10; Length 96;
Best Local Similarity 37.5%; Pred. No. 5.6e-09;
Matches 30; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAANGSGSEAYGVQVKWDATATE 64
Db 5 RYEFCAIQGAATDINSTGRINSLDGLKSLQPMVASWEGESSEAYSEAQIKWDRAAAE 64

Qy 65 LNNALQNLARTISEAGQAWA 84
Db 65 LNTILATISNTVAQGAERMS 84

RESULT 16
US-09-813-333-60
; Sequence 60, Application US/09813333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-60
Query Match      21.1%; Score 101; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAASAIQGNVTS 24
Db 1 QWNFAGIEAASAIQGNVTS 20

RESULT 17
US-10-044-703-60
; Sequence 60, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60
Query Match      21.1%; Score 101; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAASAIQGNVTS 24
Db 1 QWNFAGIEAASAIQGNVTS 20

RESULT 17
US-10-044-703-60
; Sequence 60, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-60
Query Match      21.1%; Score 101; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 QWNFAGIEAASAIQGNVTS 24
Db 1 QWNFAGIEAASAIQGNVTS 20
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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-61

Query Match      20.3%; Score 97; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAASAIQGNVTSIH 26
Db 1 NFAGIEAASAIQGNVTSIH 20

RESULT 21
US-10-044-703-61
; Sequence 61, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-61

Query Match      20.3%; Score 97; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NFAGIEAASAIQGNVTSIH 26
Db 1 NFAGIEAASAIQGNVTSIH 20

RESULT 22
US-09-804-980-175
; Sequence 175, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 175
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-175

Query Match      20.0%; Score 96; DB 12; Length 96;
Best Local Similarity 30.2%; Pred. No. 0.0056;
Matches 29; Conservative 16; Mismatches 39; Indels 12; Gaps 3;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAYQGVQKQWDA 60
Db 1 MSQIMVNPAMMAHAGDMAGYAGTQLSLGADIASEQAVLSSAWQDGTGITYQGMOTQW-- 58

RESULT 23
US-09-804-980-199
; Sequence 199, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 199
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-199

Query Match      20.0%; Score 96; DB 12; Length 96;
Best Local Similarity 30.2%; Pred. No. 0.0056;
Matches 29; Conservative 16; Mismatches 39; Indels 12; Gaps 3;

QY 1 MTEQOWNFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAYQGVQKQWDA 60
Db 1 MSQIMVNPAMMAHAGDMAGYAGTQLSLGADIASEQAVLSSAWQDGTGITYQGMOTQW-- 58

RESULT 24
US-10-156-761-10069
; Sequence 10069, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10069
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10069

Query Match      18.6%; Score 89; DB 15; Length 99;
Best Local Similarity 22.4%; Pred. No. 0.034;
Matches 17; Conservative 19; Mismatches 40; Indels 0; Gaps 0;

QY 5 QNWFAGIEAASAIQGNVTSIHSLDEGKQSLTKLAAAWGSGSSEAYQGVQKQWDA 64
Db 9 QVTYDALDEAATSIQNEAKTLEQDLQELKLVQCKQYWDGAQDAFDSKLAWDKEAD 68

QY 65 LNNALONLARTISEAG 80
Db 69 IHTALTGIGHAVGTAG 84
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Db 1 MSQIMYNYPAMLGHAGDMAGYAGTQLSLGABIAVEQAALQSAWQDGTGITYQAWQAQW-- 58
Qy 61 TATELNALQNLARTISEAGQAMAST-EGNVVTGMFA 95
Db 59 -----NOAMEDLVR-----AYHAMGSTHEANTMAMMA 85

RESULT 27
US-09-804-980-195
; Sequence 195, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 195
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-195

Query Match 17.7%; Score 85; DB 12; Length 96;
Best Local Similarity 29.2%; Pred. No. 0.089;
Matches 28; Conservative 14; Mismatches 42; Indels 12; Gaps 3;

Qy 1 MTEQQWNFAGIEAAASAIQGNVTSHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKQKWA 60
Db 1 MSQIMYNYPAMLGHAGDMAGYAGTQLSLGABIAVEQAALQSAWQDGTGITYQAWQAQW-- 58
Qy 61 TATELNALQNLARTISEAGQAMAST-EGNVVTGMFA 95
Db 59 -----NOAMEDLVR-----AYHAMGSTHEANTMAMMA 85

RESULT 28
US-10-080-170-378
; Sequence 378, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 378
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-080-170-378

Query Match 17.7%; Score 85; DB 16; Length 96;
Best Local Similarity 29.2%; Pred. No. 0.089;
Matches 28; Conservative 14; Mismatches 42; Indels 12; Gaps 3;

Qy 1 MTEQQWNFAGIEAAASAIQGNVTSHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKQKWA 60
Db 1 MSQIMYNYPAMLGHAGDMAGYAGTQLSLGABIAVEQAALQSAWQDGTGITYQAWQAQW-- 58
Qy 61 TATELNALQNLARTISEAGQAMAST-EGNVVTGMFA 95
Db 59 -----NOAMEDLVR-----AYHAMGSTHEANTMAMMA 85

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US-09-791-171-2
; Sequence 2, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-2

Query Match 17.7%; Score 85; DB 9; Length 96;
Best Local Similarity 29.2%; Pred. No. 0.089;
Matches 28; Conservative 14; Mismatches 42; Indels 12; Gaps 3;

Qy 1 MTEQQWNFAGIEAAASAIQGNVTSHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKQKWA 60
Db 1 MSQIMYNYPAMLGHAGDMAGYAGTQLSLGABIAVEQAALQSAWQDGTGITYQAWQAQW-- 58
Qy 61 TATELNALQNLARTISEAGQAMAST-EGNVVTGMFA 95
Db 59 -----NOAMEDLVR-----AYHAMGSTHEANTMAMMA 85

RESULT 26
US-09-804-980-2
; Sequence 2, Application US/09804980
; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 670001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-2

Query Match 17.7%; Score 85; DB 12; Length 96;
Best Local Similarity 29.2%; Pred. No. 0.089;
Matches 28; Conservative 14; Mismatches 42; Indels 12; Gaps 3;

Qy 1 MTEQQWNFAGIEAAASAIQGNVTSHSLDDEGKQSLTKLAAAWGSGSEAYQGVQKQKWA 60

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Query Match 16.9%; Score 81; DB 10; Length 15;

